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GenCore version 5.1.6
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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11602.436 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS TITLE	ORGANISM	KEYWORDS SOURCE	ACCESSION VERSION	RESULT 1 AB037738 LOCUS DEFINITION
1 (sites) Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which	Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	Homo sapiens (human)	AB037738 AB037738.1 GI:7243014	AB037738 5646 bp mRNA linear PRI 14-MAR-2000 Homo sapiens mRNA for KIAA1317 protein, partial cds.

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PUBMED
REFERENCE
AUTHORS
TITLE
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ORIGIN
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MEDLINE
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92.2; Score 3198.4; DB 9; Length 5646;

Best Local Similarity 99.2; Pred. No. 0;

Matches 3225; Conservative 0; Mismatches 26; Indels 1;
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603 ATGTCGGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTCCC 662
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Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
20181126
10718198
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Ohara,O., Nagase,T. and Kikuno,R.
                                                                                                                                                                                                                                                                          AATCAAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAAACTGTAGTCGTT 542
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/product="KAA1317 protein"
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/protein_id="BA92555.1"
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/note="Start codon is not identified."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fh13117"
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/clone_lib="pBluescriptII SK plus"
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Center: Washington University Genome Sequencing Center Center ode: WUGSC	2763 GTTCTTACTGCCCACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCTGT 2822
University School of Medicine, 4444 Forest Park Parkway, St. Louis MO 63108, USA COMMENT On Mar 13, 2000 this sequence version replaced gi:6652510.	2703 TCCACACTCAGCCTTCTACCCTGAACTGAATTATCACCCTTTTCTCCATGTTTTCAGA 2762
REFERENCE 2 (bases 1 to 182638) AUTHORS Waterston, R.H. TITLE Direct Submission JOHRNAL Submitfed (01-JAN-2000) Genome Semiencing Center Washington	2643 AACATTCCTTGTGTTAAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATGAC 2702
I (bases 1 (bases Waterston The sequen	2583 GGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGTCA 2642
Homo sapiens Homo sapiens Eukaryota; Met	2523 ACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTATTGTGAAATTAATACCCTCA 2582
18 unordered pieces. AC019335 AC019335 AC019335 GI:7231064 HTG: HTGS: DPAFT	2463 TGACTCTTTCTAAAATTCTTTTGGGAAGATTTCCCAGCCTTTCTTCACAACACTTTCTA 2522
RESULT 2 AC019335/c AC019335 LOCUS AC019335 DEFINITION USES CANADOSCUS 5 COLOR BELL-47771 WORKING DEAFT SECURIORS DEFINITION USES CANADOSCUS 5 COLOR BELL-47771 WORKING DEAFT SECURIORS	2403 AAGGGCTGTGCTCCCAGCAGCAGCCCTCTCTTAGAATATTTCAGATGGATG
TY 3423 ANABANANANANANANANANANANANANANANANANANA	2343 CAAGCACAACTAAGTATGTATATACACATGACGCACACGATGCCAGGGCCTAGACCTCCC 2402
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3879 ATAATTTGTCAA	2223 AATTITGGTTTTTCCTTITGTTTATGGGGGTTGGGGGGAATGGCAGATTTATATGACTTTT 2282
3243 ANGELIAMAGACCAGITITATIICAGCATICCACAGAIICAGGGGTAACCAAAAA 3819 AAGGTTAAAAAGACCAGITTTATTITCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAA 3819 AAGGTTAAAAGACCAGITTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAA	2163 CCTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTTTT 2222
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2993 IAANCIACAAAGCIACAIIIIIACIIGCIIGIAGCCGIIIIIGIIIIIIII	1863 GGAATTCATATTTTAAAGGAAAAAAATACAACTAATGATGCACATTTCTTAGAACAAT 1922
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3399 GTTCCTGTGTTGTTGTGGAACTAAGGACACACACACATACTTGAATAAGGGTCCGGCCTT	1743 GGTTTCCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATAAG 1802
Oy 2823 GTTCCTGTGTTGTTGTGGAACTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCCTT 2882	2260 CAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCCTAAAAATCAAAATTCCAGATC 2319

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/db_xref="taxon:9606"
/chromosome="5"
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2928: contig of 1635 bp in length
5126: contig of 12098 bp in length
5226: gap of unknown length
6713: contig of 12098 bp in length
6813: gap of unknown length
9443: contig of 5430 bp in length
13186: contig of 5433 bp in length
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13186: contig of 4815 bp in length
13186: contig of 4815 bp in length
13286: gap of unknown length
13286: contig of 4815 bp in length
13296: contig of 4815 bp in length
13296: gap of unknown length
13296: contig of 8652 bp in length
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                                                                                                                                                                                                                                                                                                                                                                    1516 ACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGGCCCCTGTCCAGCTGAT 1575
                                 1636 GGAATCGAACATGAGCAGCAAAAAAAAAAGCTGTTAAAGAAAAGCTCTCTAAATTGAGGAGGA 1695
                                                                                                                                      1696 GCTGGAGAAATGTATCCAGGATTTCCTAAAAAAAAAATTCCAGATCGGTTTCCTGAGAG 1755
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50969 .59100
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31709. 41973
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vector_side:right"
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	2955	2896 AGAAAGTTGTATTCCACACACAACCTAATAATTTCTTATAAAAATTTTAAAACTACAAAGC	Ş
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	2895	2836 TGTGGAACTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCCTTTTGTTTTTAG	á
COMMI	178292	178351 ACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCTGTGTTCCTGTGTTGT	ß
J01	2835	2776 ACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAGTTCTGTGTTCCTGTGTTTCT	ş
REFEI	2775 178352	2716 TTCTCTACCCTGAACTGAATTATCACCCTTTTCTCCATGTTTTCAGAGTTCTTACTGCCC	B 8
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ORC	2535 178592	2476 AAATTCTTTTGGGAAGATTTCCCAGCCTTTCTTCACAACACTTTCTAACATCAATGACT 	P Qy
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RESU ACOO LOCU	2415 178712	2356 GTATGTATATACACATGACGCACACGATGCCAGGGGCCTAGACCTCCCAAGGGCTGTGCTC	유 성
Db	2355 178772	2296 ATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAACACAAGCAGCAACTAA	<u> </u>
S B 8	2295 178832	2236 CCTTTTGTTTATGGGGGTTGGGGGGAATGGCAGATTTATATGACTTTTCACTCAAATCTAT	B &
O B 4	2235 178892	2176 GTATGGTAGAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTTTTAATTTTGGTTTTT	8 4
S R &	2175 178952	2116 GTCATTTATCCCAAACTGGGTTTTTTCTCTCATCCTTCTACCTCCCTC	Ş
S B 4	2115 179012	2056 GCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGCTGAGAGGCCTTGGGA	ß 8
S B 8	2055 179072	1996 TAGATGTGGAAGTACAAGAAAATCTTTTTAGTTATTTGTTTTGTTTACTTCGTCCCATGT	유 성
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P &	1935 179192	1876 TAAAGGAAAAAATACAACTAATGATGCACATTTCTTAGAACACAATAGTCCATTGATAT 	용 <i>성</i>
 ? B	1875	1816 CGGGGAAAAAAAAAAAAAAAAGAGTCATTTGAAATTAACCTCATAAAAGGAATTCATATTT	B &

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                                                              3256 CAGITTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTATTTGTCAAT 3315
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(bases 1 to 184589)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submitted (17-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Oct 17, 2001 this sequence version replaced gi:8122137.
Draft Sequence Produced by DOE Joint Genome Institute Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 184589)
DOE Joint Genome Institute and Stanford Human Genome Center. Finishing Completed at Stanford Human Genome Center www.shgc.stanford.edu Quality: Phrap Quality >>40 99.5% of Sequence; Estimated Total Number of Errors is 0.9. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184589)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission Homo sapiens (human) 184589 bp DNA linear PRI 17-OC Homo sapiens chromosome 5 clone CTB-85P21, complete sequence. AC008716
AC008716.7 GI:16195190 www.jgi.doe.gov 2 (bases 1 to 184589)
DOE Joint Genome Institute. PRI 17-0CT-2001

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	STGCTACAAGAAGGT TAACCAAAAAATAAT 	AGCCATCCGTCCATG STGCTACAAGAAGGT 	ACTATOTTTTCAA AGCCATCCGTCCATG	TGTAACAACCCAACA AACTATCTTTTCAA1	TGGGATTCGGGCTTT	TAAAAATTTTAAACT TGGGATTCGGGCTTT	TAAAATTTAAACT	AAGTTCTGTGTTCCT	GTTTTCAGAGTTCTT AAGTTCTGTGTTCCT 	CTÀAATGACTCCACA GTTTTCAGAGTTCTT 	AGCTGGTCAAACATT CTAAATGACTCCACA 	ATACCCTCAGGCTCC AGCTGGTCAAACATT(ATACCCTCAGGCTCC	CACTTTCTAACATCAJ	ATGAGCTTCTGACTCT 	GACCTCCCAAGGGCT	GTGCAACACAAGCAC GTGCAACACAAGCAC	TGACTTTTCACTCAA TGACTTTTCACTCAA	
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Query Match 58.8%; Score 2038.6; DB 9; Length 98360; Best Local Similarity 98.5%; Pred: No. 0; Matches 2068; Conservative 0; Mismatches 29; Indels 2; Gaps 1; Matches 2068; Conservative 0; Mismatches 29; Indels 2; Gaps 1; Oy 1336 TGTCTTCTAGGTGAGCCTTCCAGATGGTCACCTCACACTGCGATTGCTGCTGCAAGAA 1395 [Quality: Phrap Quality >=40 99.1% of Sequence; Estimated Total Number of Errors is 0.8. STS Content: STS Con	Submitted (01-SEP-2000) DOE Joint Ge Submitted (01-SEP-2000) DOE Joint Ge Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 98360) DOE Joint Genome Institute and Stanf Direct Submission Submitted (03-CCT-2001) DOE Joint Ge Drive, Walnut Creek, CA 94598, USA CON Oct 3, 2001 this sequence version Draft sequence Produced by DOE Joint www.jgi.doe.gov Finishing Completed at Stanford Huma www-shgc.stanford.edu	ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 'FERENCE 1 (bases 1 to 98360) AUTHORS Direct Submission TITLE JOURNAL Unpublished REFERENCE 2 (bases 1 to 98360) AUTHORS DOE Joint Genome Institute. AUTHORS DOE Joint Genome Institute. TITLE Direct Submission DOE Joint Genome Institute. AUTHORS Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA REFERENCE 3 (bases 1 to 98360) REFERENCE 3 (bases 1 to 98360) REFERENCE 3 (bases 1 to 98360) REFERENCE 5 (bases 1 to 98360) REFERENCE 6 (bases 1 to 98360) REFERENCE 7 (bases 1 to 98360) REFERENCE 8 (bases 1 to 98360) REFERENCE 9 (bases 1 to 98360) REFERENCE 1 (bases 1 to 98360) REFERENCE 1 (bases 1 to 98360) REFERENCE 2 (bases 1 to 98360) REFERENCE 3 (bases 1 to 98360)	73/c ACO08473 TION Homo sapiens ACO08473 N ACO08473.6 G	Db 177203 CAGTTTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAAT 177144 Oy 3316 TAATAGTTGTGGCCCAAGCACTCCTAATTTGTTTTATTGCGTGGTGGCATGTGTGTAT 3375
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2356 GTRIGHTANIACAGNICACGATACCAGGCCTAGACCTCCAAGGCCTCCAAGGCCTCCAAGGCCTAGACCTCCAAGGCCTAGACCTCCAAGGCCTAGACCTCCAAGGCCTAGACCTCCAAGGCCTAGACCACGATGCCAAGGGCCTAGACCTCCCAAGGGCTTTCTTA 2475 2416 CTGCTCCCAGCAGCCCTCTCTAGAATATTTCAGATGGATG	GTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTTTTAATTTTGGTTTTT [0-0 0-0 4-4	1756 AAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATTATAGGGAGGG		6572 CTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGCCCTGTCCAGCTGACTCCAGCTGACGCCAGCCA

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Sequence 175 from Patent WO0222660.
AX405760
                                                                                                         Homo sapiens (human)
                                                                                                                                                                        AX405760.1 GI:21438959
Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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     CTGAATACTTCCAGCTCCCAGACTTGGTCAAACTCCTGACCCCCGATGAAATCAAGCAAA
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                                                                        GGGACAGGCAGGTGGTCCTGCCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAGGGAAG 842
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RGPNSRSSPSHCDCCKNGKGDKEGESGTSCNDLSTSGSRESNMSSKKKAVKEKLSIE
EELEKCIQDFLKIKIPRFERKHFMSSELLRKYHL"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="GI:21438960"
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Produced by DOE Joint Genome Institute
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JG-1999) Production Sequencing Facility, DOE Joint
5, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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da; Primates; Catarrhini; Hominidae; Homo.
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.5%; Score 1161.8; DB 9; Length 171949;

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Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 209114)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 209114)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTC-222022, complete sequence.
ACOO8383
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGAATATGTCTTCTACCGTGAG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTCAAGCTA 170127
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Ouery Match
Best Local Similarity 99.8%; Bred. No. 1.4e-240;
Matches 1163; Conservative 0; Mismatches 2; Indels
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            168951 AGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAGAATCTG 169010
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Location/Qualifiers
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On May 1, 2001 this sequence version replaced gi:13699337
Draft Sequence Produced by DOE Joint Genome Institute
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65378 a 39329 c 40172 g 64235 t
                                        AGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAGAATCTG 966
                                                                                                                                                     ATACTTCCAGCTCCCAGACTTGGTCAAACTCCTGACCCCCGATGAAATCAAGCAAAGCCC 906
                                                                                                                                                                                                                             CAGGCAGGTGGTCCTGCCTGATCACTTTCCAGAAAAAGGGAAGACTGAAAAGGGAAGCTGA 168890
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                                                                                                                   ATACTTCCAGCTCCCAGACTTGGTCAAACTCCTGACCCCGATGAAATCAAGCAAAGCCC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson,R.K.
Direct Submission
Direct Submission
Submitted (12-JUN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jun 12, 2003 this sequence version replaced gi:21886968.
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Mus musculus chromosome UNK clone RP24-475B8, WORKING DRAFT SEQUENCE, 4 unordered pieces.
AC127249
AC127249
AC127243
AC127243
AC127243
AC127243
AC127243
AC1272493
AC1272493
AC1272491
AC1672491
AC16
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 133026 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 135132)
                                                                                                                                                                                                                                                                                  Center project name: M_BB0475B08
                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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McPherson, J.D. and Waterston, R.H.
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Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                          124386
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       1827 AAAAAAAAGAGTCATTTTGAAATTAACCTCATAAAAGGAATTCATATTTTAAAGGAAAAA 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 133293 bases at least Q30 Consensus quality: 133464 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                       GGCAGTCTGAACTTTTACGGAAGTATCATCTATAGGGGGAGGGCTGTGG------- 124278
                                                                                                                                                                                                          GTATCCAGGATTTCTTGAAGATAAAAATTCCAGATCGCTTCCCTGAGCGAAAACATCCTT 124327
                                                                                                                                                                                                                                                                          GTATCCAGGATTTCCTAMAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAACATCCTT 1766
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                                                                                                                                       GGCAATCTGAACTTTTAAGGAAGTATCATCTATAAGGGAGGCCTGGGGGCGGGGAAAAAA 1826
                                                                                                                                                                                                                                                                                                                                                 TAAGCAGCAAAAAGAAAGCTGCGAAGGAAAAGCTTCTCCATCGAGGAAGAGCTGGAGAAAT 124387
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                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGCAGCAAAAAAAAGCTGTTAAAGAAAAGCTCTCAATTGAGGAGGAGCTGGAGAAAT
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8887. .23581
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23682. ..43616
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26731 c 25600 g 38364.t
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig23"
43717. .135132
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8886: gap of unknown length
23581: contig of 14695 bp in length
23681: gap of unknown length
43616: contig of 1935 bp in length
43716: gap of unknown length
43716: gap of unknown length
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70.7%;
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Pred. No. 7.5e-174;
0; Mismatches 523;
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2919	2861 ACTTGAATAAGGGTCCGGCCTTTTGTT-TGTTTTAGAGAAAGTTGTATTCCACACACACAC	•<
2860 123206	2801 CATAATCCACATTAAGTTCTGTGTTGTGTGTTGTTGTGGAACTAAGGACAACACACAC	0 4
2800 123266	2741 CCCTTTTCTCCATGTTTTCAGAGTTCTTACTGCCCACAGTTTAATGGTGTGGCCTTTCCA	0 \
2740 123326	2681 ACAAAATTTTCTGCTAAATGACTCCACACTCAGCCTTCTCTCTC	
2680 123385	2624 GGATGAGGAGAGCTGGTCAAACATTCCTTGTGTAAAAAAATCAAACATTCATATCC	•
2623 123445	2564 TGTGAAATTAATACCCTCAGGCTCCATTTTACTGCTTTTGCTCTTTGTCTGCATTAAGAGA	•
2563 · 123505	2509 CACAACACTTTCTAACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTAT	•
2508 123565	2449 GATGGATGAGCTTCTGACTCTTTCTTAAAATTCTTTTGGGAAGATTTCCCAGCCTTTCTT	
2448 123625	2389 GGCCTAGACCTCCCAAGGGCTGTGCTCCTGCTCCCAGCAGCCCTCTCTTAGAATATTTCA	
2388 123684.	2330 TATTTGTGCAACACAAGCA-CAACTAAGTATGTATATACACATGACGCACACGATGCCAG	
2329 123744	2270 TTATATGACTTTTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAG	
2269 123804	2215 GAATTITTAATTTIGGTTTTTCCTTTTGTTTAIGGGGTTGGGGGGAAIGGCAGAT	
2214 123864	2157 CTCCCCCTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTG	
2156 123924	2123 ATCCCAAACTGGGTTTTTT	
2122 123984	2064 TCTT-ATATATATGAGAGCCAGCTACGTAAAAGTAGCTGAGAGGCCTTGGGAGTCATTT	
2063 124044	2007 GTACAAGAAATCTTTTTAGTTAGTTATTTGTTTGTTTACTTACGTCCCATGTGCTAACTA	
2006 124104	1947 CTTTACCTAGTTCACCTTAACATGTAAATCCACAGGGTAGATTTCTTTC	
1946 124164	1887 AATACAACTAATGATGCACATTTCTTAGAACACAATAGTCCATTGATATACTACTGCCTA:	
124222	124277GTAGTCGCCACTTTGAAATAAACCTCCCCAAAGGAAGACATATGTTAAAGGAAAAA	

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chang, J., Colines, S., Collymore, A., Coke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., DeArellano, K., Gadem, J., Galdan, J., Gardyna, S., Ginde, S., Gord, S., Geyette, M., Gaben, L., Grand-Pierre, N., Ginde, S., Gord, S., Geyette, M., Grabam, L., Grand-Pierre, N., Ginde, S., Gord, S., Gord, S., Kelle, C., LaRocque, K., Lamazaree, R., Kamat, A., Karatas, A., Kelle, C., LaRocque, K., Lamazaree, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., Marquis, N., Marthews, C., McCarthy, M., McCarthy, M., McHous, L., Marquis, N., Marthews, C., McCarthy, M., McCarthy, M., McHous, L., Marquis, N., Marthews, C., Norman, C., McGennan, K., Mehley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travis, N., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., W.J., Young, G., Viel, R., W.J., Young, G., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., W.J., Young, G., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., W.J., Young, G., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., W.J., Young, G., W.J., Yo
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus, Clone RP23-248F9
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Query Match 24.6%; Score 853.2; DB 2; Length 186417; Best Local Similarity 70.7%; Pred. No. 7.5e-174; Matches 1473; Conservative 0; Mismatches 523; Indels 86; Gaps 22;	/or /mo /db /cl /cl /c1 /c373 a 3	contig gap of contig gap of contig gap of gap of contig alifiers	is is a 'wo of 6 cont. nown and they, Gaps been, but the order it is an as it is an arved. 32842: 32842: 32842: 61950: 62050:	Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence submissions@genome.wi.mit.edu Contact: sequence submissions@genome.wi.mit.edu Center project name: L19035 Center clone name: 248_F_9	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Scolpaovic, N., Stubbs, M., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission JOURNAL Submitted (05-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 22, 2003 this sequence version replaced gi:30023906.	Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 186417) Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Barren, B., Nusbaum, C., Lander, B., Camarata, J., Chang, J., Choepel, Y., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Linders, T., Levine, R., Meddrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil D., Oliver, J., Deterson, K., Dunkhang, D., Herre, N.
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AC117867
AC117867.4 GI:23618130
HTG; HTGS_PHASE1; HTGS_I
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                of Molecular and Human Genetics, Bay, Bay, Lor Plaza, Houston, TX 77030, USA 3 (bases 1 to 242679) Rat Genome Sequencing Consortium. Direct Submission
                                                                                                                                                                                                                                   Submitted (11-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of il contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Center clone name: CH230-37619
Center clone name: CH230-37619
Center clone name: CH230-37619
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 180077 bases at least Q40
Consensus quality: 190770 bases at least Q20
Consensus quality: 192614 bases at least Q20
Estimated insert size: 191086; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                 organism="Rattus norv.
/mol_type="genomic DNA
/db_xref="taxon:10116"
/clone="CH230-37619"
                 /note="clone_boundary
                                                                                                                                                                                            anism="Rattus norvegicus"
_type="genomic DNA"
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contig of 2614 bp in length
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238828 CTGAGGAAGTCAAGCAAAGTCCGGATGAGTTCTGCCACAGTGACTTCGAAGATGCCTCCC 238769
                                                                                  238888 GAAGGCTGAAAAGAGAAGCTGAGTATTTCCAGCTCCCTGACCTCGTCAAACTCCTGGCCC 238829
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8953. .9899
/note="clone_boundary
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Pred. No. 1.5e-166;
0; Mismatches 166;
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239009

238949

Center: Washington University Genome Sequencing Center Center code: WUGSC WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu Center project name: M_BA0001113 FEATURES Location/Qualifiers 9 organism="Mus musculus"	Parkway: St. Louis, MO 63108, USA 3 (bases 1 to 230128) McPherson, J. D. and Waterston, R. H. Direct Submission Submitted (03-ARR-2002) Genome Sequencing Center, 4444 Forest farkway, St. Louis, MO 63108, USA 4 (bases 1 to 230128) McPherson, J. D. and Waterston, R. H. Direct Submission Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA On Apr 3, 2002 this sequence version replaced gi:16554404.	AC098707.2 GI:19909459 HTG. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Butheria; Rodentia; Sciurognathi 1 (bases 1 to 230128) McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone Unpublished 2 (bases 1 to 230128) McPherson, J.D. and Waterston, R.H. Direct Submission Submitted (31-077-2001) Genome Sequencing	Db 238468 GATTCCACATGGTGGCCTGTAACTCCTCGGTTACAGCATTTTGTCAACCAGTATACAG 238409 Qy 1305 ATGACAGATCTGGTCAACTCCTCGATACAGCATTTTGTCAACCAGTATACAG 238409 Qy 1305 ATGACAGATCTGGTCAACCTGAATATGTCTTCTACCGTGAG 1351	238648 CCAAGITTCGGAGAGITTCCCCGGATTTTGGTTTGCGGAAGGATTTCCTTGGCAAAGGAAGTTCCCTTGGCAAAGGAAGTTCCCTTGGCAAAGGAAGTTCCAAAGGAAGTTCCAAAGGAAGTTCGAAGCACCTGATCGAGCCCCAGAAAGATACACCT	945 AAGGAAGCGACACAAGAATCTGCCCCCCTTCCCTCCCTGCCCGCCC
Oy 951 GCGACACANGANTCTGCCCCCTTCCTCGCTGCCCCCCCACGGGGCTTTCA 1010	771 TGGACTATCTCAGGGACGGGGGGTGGTCCTGATCACTTTCCAGAAAAAGGAAGAC	176 176 176	Oy 364 TCTTGGGGGAA	Db 176288 AGACAGACCTCTGAGTAACTGGGCATTTTGCCTTCTTGCCTACAGAGCCTAATGAAAT 176347 Qy 247 TGGATATAGACGAGTTATATTTTATGAAGTAGCAGCTCACTACCACCAT 303	/mol_type="genomic DNA" /db_xref="taxon:10090" /db_xref="taxon:10090" /clone="RP23-1113" BASE COUNT 69218 a 47164 c 45440 g 68306 t ORIGIN Query Match Best Local Similarity 83.1%; Pred. No. 6.8e-165; Best Local Similarity 83.1%; Pred. No. 6.8e-165; Matches 982; Conservative '0, Mismatches 172; Indels 27; Gaps 4; Qy 187 ATACGGACATTTGAGTAACTGGGGGAATTTGGCCTTGCATGTGAGCTTGATGGAAAAT 246

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RESULT 12
AC112599
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RS Milen, C., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, W., Aoyagia, A., Ayodeji, M., Baca, E., Baden, H., Balawin, D., Bandarnanike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, N., Bandarnanike, D., Barber, M., Barnstead, M., Benahmed, F., Eiswalo, D., Bandarnanike, D., Barber, M., Barnstead, M., Benahmed, F., Eiswalo, N., Cher, C., Cox, C., Cox, R., Chen, R., Cadderon, E., Charden, S., Burch, P., Burrell, K., Cadderon, E., Charden, S., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Davia, R., Deramo, C., Ding, Y., Dinh, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Garner, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, G., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, G., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, C., Kait, C.L., Lobow, H., Levan, J., Idlebido, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kaipathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kait, C.L., Lobow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lope, J., Love, J., Liu, J., Liu, Y., London, P., Longacre, S., Lope, J., Moore, S., Mandard, M., Martin, R., Parks, K., Pasternak, S., Parks, K., Pasternak, S., Parks, K., Pasternak, S., Cherer, S., Scott, G., Shatsman, S., Shen, H., Shen, H.
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC112599.4 GI:23266003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 249703)
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 249703: contig of 249703 bp in length.
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Center project name: GRQN:

Center clone name: CH200-11JA20

Center clone name: CH200-11JA20

Assembly program: Phrap; version 0.990329

Consensus quality: 233268 bases at least Q40

Consensus quality: 235949 bases at least Q30

Consensus quality: 237476 bases at least Q30

Consensus quality: 237476 bases at least Q30

Satimated insert size: 261159; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                        /note="wgs_end_extension
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Matches 1420; Conserv
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2181 GTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTTTTAATTTTGGTTTTTCCTTT
                                                                                                                                                                                                           2062 TATCTT-ATATATAATGAGAGCCAGCTACGTAAAAGTAGCTGAGAGGCCTTGGGAGTCAT 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATCTGAACTTTTAACGAAGTATCATCTATAACGGAGGGCTGGGGCGGGGGAAAAAA 1826
                                                                                                  AATCTTAAGGTTCAAGGAGAACCAGCTACGTGAGTAGCTCGAATCCCAAACCTGCTTTTT 159907
                                                                                                                                                                                                                                                           CCAGAAGCGATGCCCTTATGCTGTCCTCTGTCTCTTATTTACTTGGTCCCATGTGTTGAG 159847
                                                                                                                                                                                                                                                                                           GTACAAGAAAATCTTTTTTTAGTTATTTGT-----TTGTTTTACTTCGTCCCATGTGCTAAC 2061
                                                                                                                                                                                                                                                                                                                                                   TA-ACAACTAACAATCCATATGTGTTAGAACACAAT-GTCCATTGATGTCCTACTGCCTA 159727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATACAACTAATGATGCACATTTCTTAGAACACAATAGTCCATTGATATACTACTGCCTA 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAAAGAGTCATTTTGAAATTAAACCTCATAAAAGGAATTCATATTTTTAAAGGAAAAA 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCCAGGATTTCCTGAAGATAAAAATTCCAGATCGCTTCCCTGAGAGAAAAACATCCTT 159565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCCAGGATTTCCTAAAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAAACATCCTT 1766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATCCAGACTCTGGACCGGCCCATCAAGAAAGGCCCCGTGCAGCTGATCCAACAGTCAG 159385
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69486 a 47001 c 47902 g 74288 t 11026 others
                                                                          TGTTTGTTTTGTTTTCCTCATTTTCTGCCTCCTTCC-CTTGACCAAGAATGGACA 159966
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/note="clone_boundary
clone_end:Sp6
site:EcoRI
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        161031 AAAGACAACTTTTAATTTTCAGCATTCCTCATATATCTCAGTGGTAACTGAAAAAAGACGA 161090
                                                                                                                                                                                        160912 TAGTCCTGÁCCTGTÁTÁGÁTÁCCATCCAÁÁÁGAAATTGTGAACÁ-CTGTCTATCCATGTG 160970
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                                  3250 AAAGACCAGTTTT-ATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATT 3308
                                                                                                                                                                                                                                3130 ACATCCTGACTTGTATAGACACAGCCAAAAAGAAACTGTTAATAGCCATCCGTCCATGTA 3189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2891 TTTAGAGAAAGTTGTATTCCACACACCAACCTAATTATTTCTTATAAAAATTTTTAAACTAC 2950
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                                                                                                ACTOTGTCATCTATTAATCTACCAGTAGTTCTTCTGTTCACCTGTGTTAAAAGAATGTCC 161030
                                                                                                                                                                                                                                                                                GGTGACTGGAACATAAAGGTTTCTAATTTGATTTTTTA-----AACTTTTTTTAA 16091
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                                                                                                                                   ACTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTA 3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Red. Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                    1347 GTGAGCCTTCCAGATGGTCACCCTCACACTGCGATTGCTGCTGCAAGAATGGCAAAGGTG 1406
101
                                                                     463;
                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at: http://image.llnl.gov Series: IRAL Plate: 46 Row: g Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian Submitted (51-MAR-2003) National Concer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC049734.1 GI:29436685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa;
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                                                                                   Similarity
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                                                                   Conservative
                                                                                                                                                                                       /organism="Mus musculus"
/mol type="mRNA"
/db xref="teaxon:10090"
/clone="IMAGE:6771233"
/tissus type="Testicle, mc/clone_Tib="NIH MGC_169"
/lab_host="DH10B"
                                                                                                                                                        /note="Vector:
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                   10.6%;
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Pred. No. 8.5e-69;
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                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                   Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 175059)
                                                                                                                                                                                                                                                                                                                                                     Mclaren,S
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1827 АЛАЛАЛАЛАGGATCATTTTGAAATTAACCTCATAAAAGGAATTCATATTTTAAAGGAAAAA 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1887 AATACAACTAATGATGCACATTTCTTAGAACACAATA 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1407 ACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGACCTCTCCACATCTAGCTGCGACAGCC 1466
Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 9, 2003 this sequence version replaced gi:29825826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX323465.4 GI:31559295
HTG; HTGS PHASSI; HTGS PRAFT; HTGS_FULLTOP
Danio rerio
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX323465 175059 bp DNA linear HTG 06-JUN-2003 Danio rerio clone DKEYP-9C6, *** SEQUENCING IN PROGRESS ***, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATCCAGGATTTCCTAAAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAAAATCATCCTT 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACA---AAGGAGAGAGCGGCACCTCCTGCAATGACCTGTCCACTTCCAGCTGTGACAGCC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAGTCTGAACTTTTACGGAAGTATCATCTATAGGGGGAAGGCTGTGG------ 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATCCAGGATTTCTTGAAGATAAAAATTCCAGATCGCTTCCCTGAGCGAAAACATCCTT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGCAGCAAAAAGAAAGCTGCGAAGGAAAAAGCTCTCCATCGAGGAAGAGCTGGAGAAAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATGCGGCGGAAAAGCGACTTACTCCGGATTCTGACTTCAGGCTCCAGGGAATCGAACA 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTCAGAGGCCAGCTCTCCGCAGGAGACGGTGATCTGTGGGCCCTGTAACGCGCCAGAGCA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCATCTGTGGTCCCGTGACACGCCAGACCA 1526
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127701 ÄATGGCCCTGACTGAAAATTGCAGGACTTATCAAACGCCCAAGGACAGTGGATGTGCTCA 127760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574 CAACTCCTTCCCTGAGGTGGTAGAGCTGAATGTCGGGGGTCAAGTTTATTTTACTCGCCA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coverage: 10.15x in Q20 bases; agarose-fp
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                                                                                                                                               TCTCTTTAGGTACGTGCTGGACTATCTCCGCGATAAGACTGTCGTCCTGCCGGATTATTT 128000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATTTCTAACGACCTCACGCAGGACATCAAGGGACGCTACTTCATCGACCGGGACGGATT 127940
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                                                                                                                                                                                                        AATCCT-----AAACCCAGATGATTATAGTCACAGTGATTTTGA 128099
                                                                                                                                                                                                                                                                                                                   ACTCCTGACCCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGCCACAGTGACTTTGA 933
                                                                                                                                                                                                                                                                                                                                                                                   TCCGGAGAAGGGGAGGCTGAAACGCGAAGCTGAGTTTTTTCCAGCTGCCCGAGCTCGAA 128060
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCAA 873
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172825. 175059
/note="assembly fragment:01078"
1 30793 c 31197 g 56126 t 20
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44766. .172724
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-9C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:01355
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44765: gap of 100 bp
172724: contig of 127959 bp in length
172824: gap of 100 bp
175059: contig of 2235 bp in length.
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AUTHORS
TITLE
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ORGANISM
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VERSION
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BX470157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 198546 bases at least Q40
Consensus quality: 199010 bases at least Q30
Consensus quality: 199314 bases at least Q30
Consensus quality: 199314 bases at least Q20
Insert size: 199767; sum-of-contigs
Insert size: 201190; 3.3% error; agarose-fp
Quality coverage: 5.95x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 5, 2003 this sequence version replaced gi:30349786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX470157 200467 bp DNA linear HTG 05-MAY-2003 Danio rerio clone CH211-119P14, *** SEQUENCING IN PROGRESS ***, 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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      9515
9615
14583
14683
18934
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9514: contig of 9514 bp in length
9614: gap of 100 bp
14582: contig of 4968 bp in length
14682: gap of 100 bp
18933: contig of 4251 bp in length
19033: gap of 100 bp
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Best Local Si Matches 533; Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                          147666 TCTCTTTAGGTACGTGCTGGACTATCTCCGCGATAAGACTGTCGTCCTGCCGGATTATTT 147725
                                                                                                                                                                                                                                                                                147606 CATTTCTAACGACCTCACGCAGGACATCAACGGACGCTACTTCATCGACCGGGACGGATT 147665
                                                                                                                                                                                                                                                                                                                                                                                                                                                147546 TGTCACCCTCACCAGTGTGCCAAACTCACTGCTGGGTAAATTGTTCTCCTCTAAAAAAGA 147605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147486 GAGTTGCTCTTCTGATGTGGAGCTCAATGTAGGTGGACAGGTGTACTACACTCGCCA 147545
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                                                                                                                                                                                                                                                                                                                                             694 CACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGACAGAGATTGGATT 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634 TTCCACATTGATAAGCATCCCTCATTCCCTCCTGTGGAAAATGTTTTTCCCCAAAGAGAG 693
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814 TCCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCAA 873
                                                                                                                                                                                       574 CAACTCCTTCCCTGAGGTGGTAGAGCTGAATGTCGGGGGGTCAAGTTTATTTTACTCGCCA 633
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19034 . 66645
/note="assembly_fragment:00199
^~~mment_chain:1"
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193855. 200467
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9615, 14582
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14683, .18933
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fragment_chain:2
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fragment_chain:2"
113862. 193754
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fragment_chain:1"
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ragment_chain:1
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/clone_lib="CHORI-211"
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mol_type="genomic DNA"

db_xref="taxon:7955"
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1294 148179	1234 148119	1174 148059	1114 147999	1054 147944	994 147885	934 147825	874 147786	147726
CCAATATACAGATGACAAGATCTGGTCAAGCTACACTGAATATGTCTTCTACCGTGAG 1351	GTCAGAGTGTGGATTCCACATGGTGGCCTGTAACTCATCGGTGACAGCATCTTTCATCAA 1293 	AAGATACACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGATATGTT 1233 	GGCAAAAGAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCAGA 1173 	1054 ACAGGCAGATGCCAAGTTTCGGAGAGTTCCCCCGGATTTTGGTTTGTGGAAGGATTTCCTT 1113	CCGCAAGTGGGGTTTCATTACTGTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGGG 1053	AGATGCCTCCCAAGGAAGCGACAAGAATCTGCCCCCCTTCCTT	ACTCCTGACCCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGGCACAGTGACTTTGA 933 	147726 TCCGGAGAAGGGGAGGCTGAAACGCGAAGCTGAGTTTTTCCAGCTGCCCGAGCTCGTCAA 147785

Search completed: September 6, 2003, 06:58:49 Job time: 12244 secs

Scoring table: Sequence: Title: Perfect score:

OM nucleic

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Post-processing: Minimum Match 0% Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nimum DB seq length: 0 ximum DB seq length: 2000000000
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1: /cgn2_6/pcodata/1
2: /cgn2_6/pcodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-821-994-63
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US-09-126-0128-19
US-08-820-678A-29
US-08-820-128-09
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Sequence 66, Applisequence 706, Applisequence 114, Applisequence 63, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 3, Applisequence 22, Applisequence 22, Applisequence 22, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 26, Applisequence 27, Applisequence 28, Applisequence 29, Applisequence 29, Applisequence 31, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
ITILE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT PILICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 66
LENGTH. 664
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAMEXEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (63)
OTHER INFORMATION: n equals a,t,g, or c
US-09-904-615-66
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US-09-904-615-66
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         RESULT 2
US-09-328-965-1
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Patent No.
                                                                                                                                                         3357 TGTGTGTGCATGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAA 3416
                                                                                                                                                                                                                                                                                                                                                                                             3297 CAAAAAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCG 3356
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                                                                                                                        Application US/09904615
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US-09-202-904A-13
US-09-370-838-151
US-09-371-838-151
US-09-344-441-2
US-08-123-934A-5
US-08-123-934A-5
US-08-243-323-1
US-09-96-243-288
US-09-461-325-93
US-09-461-325-93
US-09-96-7135-1
US-09-96-713-1
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Sequence 13, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 128, Appli
Sequence 128, Appli
Sequence 178, Appli
Sequence 1, Appli
Sequence 302, App
Sequence 178, App
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Gaps

69 69

Match

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67. 68 67. 6 67. 6

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GENERAL INFORMATION:

APPLICANT: NewIns, Donald J.

APPLICANT: NewIns, Carl

APPLICANT: The Regents of the University of California

ITLE OF INVENTION: Endo- and Exo-Glucanases and Gene

FILE REFERENCE: 023070-096600US

CURRENT APPLICATION NUMBER: US/09/328,965

CURRENT FILING DATE: 1999-06-09

EARLIER APPLICATION NUMBER: US 60/088,780

EARLIER APPLICATION DATE: 1999-06-10

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-328-965-1
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FITLE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
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Matches 108;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TENGTH: 1091
TYPE: DNA
ORGANISM: Zea mays
PERATURE:
OTHER INFORMATION: maize coleoptile endo-1,3;1,4-beta glucanase cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: (68)..(979)
LOCATION: (68)..(979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              918 TAATTTCCCTCATTTTTTTTGTCTCTATGTATTTCTTTTCTTTTTCTTTTTGCTTTTTAT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       978 ĠATCĠCAATAÁAĠŤTCÄGTÁGGĠĠŤÁAAÁÁÁAAAĀAAAAAAAAAÁAÁAAAAAAAAAAAAA 1037
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ben, Feiyan
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Zhou, Ping
                                                                                                                                                                                                                                                                                                                                     Wehrman, Tom
Xue, Aidong J.
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2515)..(3519)
US-09-620-312D-706
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 706
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Best Local Similarity
Matches 128; Conserv
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
PILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-6-16
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4055
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 GTGTACAACACAGCATTTTCTGTTAAATTATTATTGGTTTTCAGTTGTAATTTGGTATTT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 AAAAGCAAAATGTGTTTTCAGATTTGTTACTTTAATAAAGGTTATCCATACCAATAAAAA 441
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                                                                                                                                                                                                                                      Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                 Napier, Mary A.
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nilarity 58.4%;
Conservative
                                                                                                                                                                                                                                                                                              Daniel
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No. 20, 20, 20, 20, 20, 20, 20, 20, 20, 20,		*** *** *** *** *** *** *** *** *** **	
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APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION	FILING DATE APPLICATION FILING DATE FILING DATE FILING DATE FILING DATE FILING DATE FILING DATE APPLICATION APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE FILING	REPLING DATE REPLING DATE REPLIATION FILING DATE REPLICATION FILING DATE REPLICATION REPLICATION REPLICATION FILING DATE REPLICATION REPLI	FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE FILING DATE FILING DATE FILING DATE FILING DATE FILING DATE APPLICATION FILING DATE APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE APPLICATION
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ICR PILLING DATE: 1997-11-13
IOR PILLING DATE: 1997-11-12
IOR FILLING DATE: 1998-01-12
IOR FILLING DATE: 1998-02-25
IOR APPLICATION NUMBER: 60/078910
IOR FILLING DATE: 1998-02-25
IOR PILLING DATE: 1998-03-20
IOR PILLING DATE: 1998-05-28
IOR APPLICATION NUMBER: 60/08760
IOR FILLING DATE: 1998-05-28
IOR APPLICATION NUMBER: 60/08760
IOR FILLING DATE: 1998-05-28
IOR APPLICATION NUMBER: 60/08760
IOR PILLING DATE: 1998-06-02
IOR APPLICATION NUMBER: 60/08760
IOR FILLING DATE: 1998-06-02
IOR APPLICATION NUMBER: 60/08760
IOR FILLING DATE: 1998-06-02
IOR PILLING DATE: 1998-06-04
IOR APPLICATION NUMBER: 60/08025
IOR FILLING DATE: 1998-06-05
IOR APPLICATION NUMBER: 60/08025
IOR FILLING DATE: 1998-06-05
IOR APPLICATION NUMBER: 60/08026
IOR APPLICATION NUMBER: 60/08

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RESULT 5
US-08-821-994-63
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APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TITLE OF INVENTION: Promoters
FILE REFERENCE: PDD 50108
FILE REFERENCE: PDD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
FORTMADE: DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Brassica napus US-08-821-994-63
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWILL
; SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR PILING DATE: 1998-07-09
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Best Local
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                                                                                                                                                                                                                                              Matches 143;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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FILING DATE: 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3345 TGTTTTATTGCGTGTGTGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGA 3404
                                  1229 ATGTATAGTATTTCGAAAAAATTGATTCACCATAGGGATTTÄATCTGTATÄAATCTCTA 1288
                                                                                                                    3203 CTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAGACCAGTTTT 3262
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TGTTGGTCAATATCATTTCAATAGAATATTTGCTTTTGGCTTGATTATGTATTAAGAG 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08821994A
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                                                                                                                                                                                                                                            2.0%; Score 69.2; DB 3; Length 1441; 53.8%; Pred. No. 4.5e-07; rative 0; Mismatches 123; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 71.2; DB 4; Length 1701; 73.4%; Pred. No. 1.6e-07; ative 0; Mismatches 33; Indels 0;
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Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Re-BEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: /desc = "mouse PAL cDNA"
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TITLE OF INVENTION: NOVEL SHC BINDING PROTEIN
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Score 69.2; DB 4; Length 2246; 64.2%; Pred. No. 5.4e-07; Indels 0;
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RESULT 7 US-09-083-587-3

Sequence 3, Application US/09083587; Patent No. 6492138; GENERAL INFORMATION:

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US-09-083-587-3
                                                                                                                                                                                                                                                                US-09-594-506-37; Sequence 37, Application US/09594506; Patent No. 6512164
                                                                           GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, J. Antoni
TITLB OF INVENTION: Thiamine Biosynthetic En:
FILE REFERENCE: BB1372 US NA
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 05/139,556
PRIOR APPLICATION NUMBER: 05/139,556
PRIOR APPLICATION NUMBER: 06-16
PRIOR FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Microsoft Office 97
; ORGANISM: Triticum aestivum US-09-594-506-37
                                              SOFTWARE: M
SEQ ID NO 37
LENGTH: 240
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ANAME: Clough, David W.
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schmand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/083,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                2406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 2246 base pairs
nucleic acid
EDNESS: single
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schmandt, et al. VENTION: NOVEL SHC BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69.2; DB 4; Length 2246; Pred. No. 5.4e-07; O; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01017/34451
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Best Local S
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Patent No.
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Best Local
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APPLICANT: WORKHING, Layo O.
APPLICANT: OFFICE OF, ENGLY M.
APPLICANT: OFFICE OF, METAPOLIC ENZYMES
TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
TILE REFERENCE: BB1322 US NA
CURRENT APPLICATION NUMBER: US/09/465,558
CURRENT FILING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,734
EARLIER FILING DATE: 1998-12-18
NUMBER OF SEO ID NOS: 70
SOFTWARE: Microsoft Office 97
SEQ ID NO 59
LENGTH: 2002
TYPE: DNA
ORGANISM: Glycine max
ORGANISM: Glycine max
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KELLY, ROSEMARIE
APPLICANT: REGISTER, ELIZABETH A
APPLICANT: WASUREKAR, PRAKASH S
APPLICANT: WASUREKAR, PRAKASH S
TITLE OF INVENTION: PSC REDUCTASE GENE FROM ZALERION
TITLE OF INVENTION: ARBORICOLA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERCK & CO., INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3243 AAGGTTAAAAGACCAGTTTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAA 3302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2239 TGTCCTGTGTÄÄTTTÄCTTTTTACACCTÄTCCTTGTACÄTATTTCTATÄTAAGTAGAATA 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3303 ATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTGTG 3362
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                                                                                                                                                                                                            , Application US/08665716
5789222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69.2; DB 4; Length 2406; Pred. No. 5.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 4; Length 2202; pred. No. 6e-07;
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SEQ ID NO 22
LENGTH: 1736
TYPE: DNA
ORGANISM: Ctenocephalides felis
FEATURE:
NAME/KEY: CDS
LOCATION: (159)..(1553)
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US-09-182-816-22
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; NAME/KEY: CDS
; LOCATION: 47..960
US-08-665-716-1
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ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TOM PC compatible
COMPUTER: TOM PC compatible
COMPUTER: TOM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMEER: US/08/665,716
FILING DATE: 23-UN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Appl Patent No. 614354
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                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/182,816
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                              APPLICANT: Wisnewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-CL
TITLE OF INVENTION: PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 908-594-5493
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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Local Similarity 75.9%; Score 68.8; DB 1, Length 1147;
Local Similarity 75.9%; Pred. NO. 5.1e-07;
1es 85; Conservative 0; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1147 base pairs
TYPE: nucleic acid
STANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3357 TGTGTGTGCATGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAA 3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021 TGCGTAGACACGTCCAAGGAGTTCTGGGGTATAAAAAGTTGTTCATTTATGAAAAAAA 1080
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APPLICANT: Wisnewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Solver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-CL
CURRENT APPLICATION NUMBER: US/09/182,816
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER PTLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 1736
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US-09-182-816-24/c
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US-09-471-528-22
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GENERAL INFORMATION:
APPLICANT: Wisnewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-C1-1
CURRENT APPLICANTION UNMEER: US/09/471,528
CURRENT FILING DATE: 1999-12-27
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Best Local Similarity 62.6
Matches 107, Conservative
                                                                                                                                                                                              Sequence 22, Application US/09471528 Patent No. 6153397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/09182816
Patent No. 6143542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1736
TYPE: DNA
ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3298 AAAAAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTTATTGCGT 3357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3358 GTGTGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAA 3417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%; Score 68.6; DB 3; Length 1736; ilarity 62.6%; Pred. No. 6.8e-07; Conservative 0; Mismatches 64; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-471-528-24
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                                                                                                                                                                                                          Query Match 2.0%; Score 68.6; DB 3; Length 1736; Best Local Similarity 62.6%; Pred. No. 6.8e-07; Matches 107; Conservative 0; Mismatches 64; Indels 0
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EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                    EQ ID NO 24
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/471,528
CURRENT FILING DATE: 1999-12-27
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
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ORGANISM: Ctenocephalides felis
FEATURE:
FEATURE:
LOCATION: (159)..(1553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPPLICANT: 10, Katherine C.
NPPLICANT: Brandt, Kevin S.
NITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
TILE REFERENCE: FC-3-C1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Wisnewski, Nanc
PPLICANT: Silver, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1565 AATAAATTATTTGTGATAATAATATATGTTAAAAATGTAAATGTAATTACTGTGAAATAAA 1624
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       3358 GTGTGTGCATGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAA 3417
                                                                                                                         172 AATAAATTATTTGTGATAATAATATAATGTTAAAAATAAATGTAATTACTGTGAAATAAA 113
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                                                  24, Application US/09471528
o. 6153397
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PILLE REFERENCE: FC-3-C1-1
CURRENT APPLICATION NUMBER: US/09/634,530
CURRENT APPLICATION NUMBER: 000-08-08
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR APPLICATION NUMBER: 09/182,816
PRIOR PPLICATION NUMBER: 09/182,816
PRIOR PPLICATION NUMBER: 09/89,510
PRIOR APPLICATION NUMBER: 08/989,510
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US-09-634-530-22
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LOCATION: (159)..(1553)
US-09-634-530-22
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 22
LENGTH: 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/09634530 Patent No. 6290958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-C1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Ctenocephalides felis
                                           1565 AATAATTATTTGTGATAATAATATAATGTTAAAAATAAATGTAATTACTGTGAAATAAA 1624
                                                                                                                                                                                                                                           3298 AAAAAATTAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGT 3357
                                                                                               INFORMATION:
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Patentin Ver. 2.0
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Search completed: September 6, 2003, 08:48:45
Job time : 227 secs

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Result
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Perfect score:
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Maximum Match 100%
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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9541.055 Million cell updates/sec
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Match Length:DB
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14 US-10-056-884-1

14 US-10-056-884-3

14 US-10-060-036-4467

14 US-10-060-036-564

14 US-10-080-980-8

14 US-10-080-980-8

10 US-09-918-995-2311

14 US-10-056-884-8

10 US-09-834-975-45-1

10 US-09-834-975-45-1

11 US-10-106-689-1525-1

12 US-10-106-689-1525-1

14 US-10-106-6861-9

US-09-770-444-872-1

15 US-09-770-444-872-1

15 US-09-970-254-66
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Sequence 1, Appli
Sequence 4467, Ap
Sequence 564, Appli
Sequence 1, Appli
Sequence 2311, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 112, Appli
Sequence 112, Appli
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                                                                                                                                                                                                                                                             Matches 3468;
                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KBY: CDS
LOCATION: (515)..(1798)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
        121 GATCTGGCAGCTCTGTGTATTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA 180
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2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	
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٠.	•	17, Appl	17, Appl		17, Appl	Ü	1594, Ap	47, Appl	·U	8434, Ap		3918, Ap	24, Appl		13, Appl	8503, Ap	11420, A	95, Appl	95, Appl	37095, A	23, Appl	31149, A	1482, Ap	706, App	N	•	66, Appl	

Sequence 1, Application US/10056884
Publication No. US20030032786A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SU)
TITLE OF INVENTION: K-BetaM2
FILE REFERENCE: D0076 NP
CURRENT APPLICATION UNMBER: US/10/056,884
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PRIOR APPLICATION UNMBER: US 60/263,872
PRIOR FILING DATE: 2001-01-24
PRIOR PRIOR PRIOR DATE: 2001-01-24
PRIOR PRIOR PRIOR DATE: 2001-01-24
PRIOR PRIOR DATE: 2001-01-24
PRIOR PRIOR DATE: 2001-01-24
PRIOR PRIOR DATE: 2001-01-24
PRIOR PRIOR DATE: 2001-01-34
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 3468 1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAGTTGTGCCCAGAAAATTATGGT 60 1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAAGTTGTGCCAGAAAATTATGGT 60 TTGAACATGGGCAGTTTTCTCCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGGA 120 TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGGA 120 Conservative 100.0%; Score 3468; 100.0%; Pred. No. 0; 0; Mismatches DB 14; Length 3468; 0; Indels 0; Gaps

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CATCCAGGGTTTAAACTACTTTTCAGGATTAGAGGAGGTCATTTTTTATATAGGTTAGCATTCATT	
B	2 0 0 0 0 0
1391 Tricciscrochaghartsgeanagegaagagagagagagagagagagagagagagaga	ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGC CTGTAACTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC [

Db 541 AAGATGCCTACCAAGGAAGCGACACAGAAGCATCCTGCCACCTTGGGCAGAGAGGG 1052	7 3361 TGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAAAA	용 성
ANCARGOCCOCCAGA MAGA ANGA GA GA ANGA GOCCAGA TOTA CONTROLL AND ANCARGOCCAGA GA GA ANGA GA G	3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG 3360	유
	2241 AGAAGGTTAAAAGACCAGTTTTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAA 3300	음 성
361 TCTTGTTCCGTTATATTCTGGACTATCTCAGGGACAGGCAGG	3181 GTCCATGTAACTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACA 3240	8 8
301 ACACCECTATION CONTROL CONT	3121 TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAAACTGTTAATAGCCATCC 3180	유 성:
63 ATT CACATTANIANGATICCTICATICCTICTICS AND	3061 ACCCAACAAGGTAACTGAAGCTCCAGAGTTAAGGTTTCAGATTTCTAAATGAAACTATCT 3120 	₹
181 CCAACTCCTTCCCTGAGGTGGTAGAGCTGAATGTCGGGGGTCAAGTTTATTTTACTCGCC	3001 CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCATTTTTATGATGTCTGTAACA 3060	문 왕.
	2941 TTTAAACTACAAAGCTACATTTTTACTTGCTTGTAGCCGFTTTTGTTTTG	음 성
	2881 2881	유 성
	2821 GTGTTCCTGTGTTGTTGTGGAACTAAGGACACACACACAC	음 성
Best Local Similarity 100.0%; Pred. No. 2.1e-172; Best Local Similarity 100.0%; Pred. No. 2.1e-172; Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	2761 GAGTTCTTACTGCCCACAGTTTAATGGTGTGGGCCTTTCCACATAATCCACATTAAGTTCT 2820	유왕
Hon 3	2701 ACTCCACACTCAGCCTTCTCTACCCTGAACTGAATTATCACCCTTTTCTCCATGTTTTCA 2760	B &
; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 3 ; LENGTH: 769 ; TYPE: DNA	2641 CAAACATTCCTTGTGTTAAAAAAATCAAACATTCATATCCACAAAATTTTTCTGCTAAATG 2700 	S
PRIOR FILING DATE: 2001-01-24 ; PRIOR APPLICATION NUMBER: US 60/269,794 ; PRIOR FILING DATE: 2001-02-14 ; PUMBER OF SEO ID NOS: 73	2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640	B 8
FILE REFERENCE: D0076 NP ; CURRENT APPLICATION NUMBER: US/10/056,884 ; CURRENT FILING DATE: 2002-01-24 ; PRIOR APPLICATION NUMBER: US 60/263,872	2521 TAACATCAAATGACTCTCATCAACAAATTGTATTCCTTATTGTGAAATTAATACCCT 2580 	유 성
	2461 TCTGACTCTTTCTTAAAATTCTTTTGGGAAGATTTCCCAGCCTTTCTTCACAACACTTTC 2520	음 성
RESULT 2 US-10-056-884-3 : Sequence 3, Application US/10056884 : Publication No. US2003003786A1	2401 CCAAGGGCTGTGCTCCTGCTCCCAGCAGCCCTCTCTTAGAATATTTCAGATGAGATGAGCT 2460	음 성
Qy 3421 АЛАДАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА	2341 CACAAGCACAACTAAGTATGTATATACACATGACGCACGC	유정

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TI: Briscol-Myers Squibb Company
TI: Briscol-Myers Squibb Company
INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUI
INVENTION: K-betam2
ERENCE: D0076 NP
ERENCE: D0076 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
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AAGATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCTTCCTCCCTGCTGCCG 992
                                                                                                                                                                 AACTCCTGACCCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGCCACAGTGACTTTG 932
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                                                                                                                                                                                                                                                                                                                                   TTCCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCA 480
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APPLICANT: MENSON, DAXIN R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION MUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 4467
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US-10-060-036-4467
; Sequence 4467, Application US/10060036
; Publication No. US20030073144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
NAME/KEY: misc_feature
LOCATION: 552, 569
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-4467
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US-10-060-036-564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                          Sequence 564, Application US/10060036 Publication No. US20030073144A1 GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1113 TGGCAAAAGAACTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCCTGA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1053 GACAGGCAGATTCCCAAGTTTCGGAAGATTTCCCCGGATTTTTGGTTTTGTGAAGGATTTCCT 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 GACAGGCAGATGCCAAGTTTCGGAGAGTTCCCCCGGATTTTTGGTTTGTGGAAGGATTTCCT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3206 AGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAAGACCAGTTTTATT 3265
                                                                                                                                                                                                                                                                                                                                                                                                             3326 GTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTGTGTGCATGTGTGTATGTGTATCACA 3385
                                                                                                                                                                                                                                                                                                                         195
                                                                                                                                                                                                                                                                                                                                                                               15 AGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAAGACCAGTTTATT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 TTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGT 134
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                                                                                                                                                                                                                                                                                              GGTAATAAAGGCAATTGGATGATATCTGTAGGAGGAAAAACAATGACTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 205; DB 14; Length 632; pred. No. 2.2e-38; 0; Mismatches 15; Indels
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TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 564
LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 534, 551, 575, 576
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-060-036-564
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US-10-080-980-1
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                                                                                                                                                                                                                         FEATURE:
, NAME/KEY: CDS
, LOCATION: (121)..(1095)
US-10-080-980-1
                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION NUMBER: US/1080980

Fequence 1, Application US/1080980

Publication No. US20030036115A1

GENERAL INFORMATION:
APPLICANT: Briscol-Myers Squibb Company
APPLICANT: Briscol-Myers Squibb Company
APPLICANT: D10121 NP
FILE REFERENCE: D0121 NP
FILE REFERENCE: D0121 NP
CURRENT APPLICATION NUMBER: US/10/080,980
CURRENT APPLICATION NUMBER: US/10/080,980
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR APPLICATION NUMBER: US 60/278,953
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 74
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Best Local Similarity 93.3%;
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                                                                                                                                              Query Match
Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                              LENGTH: 2052
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3210 ACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAGACCAGTTTTATTTTGA 3269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3330 CAAGCACTCCTAATTTGTTTTATTGCGTGTGTGTGTGCATGTGTATGTGTATCACAGGTA 3389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3270 GCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGTGTGC 3329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 caadcactcctaatttgttttattdcgtgtgtgtgcatgtgtgtgtatgtgtatcacacgta 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ÁTAÁAGGCAÁTTGGATGATATCTGTÁGGÁGGÁÁÁÁÁÁÁÁÁTGÁCTÁÁ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGTGTGC 120
1027 AGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGTTCCCCG 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Accahinagereritichtadacerigigeracaagaaggitaaaaagaceagiitiatitica 60
                                                              705 CACGCCGTCCCAGTCGCTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCG
                                                                                                     967 ccccccrrcccrcccrcccrcccrqcccaAccccAAGTGGGGTTTCATTACTGTGGGTTACAG 1026
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                                                                                                                                                   Conservative
                                                                                                                                              4.8%; Score 167; DB 14; Length 2052; 64.6%; Pred. No. 4.8e-29; ative 0; Mismatches 140; Indels 6.
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pred. No. 1.9e-37; 
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bristol:Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE RECODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
TITLE OF INVENTION: K-betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
FILE REFERENCE: D0121 NP
FILE REFERENCE: D0121 NP
FILE REFERENCE: D0121 NP
FILE REFERENCE: D0121 NP
FILE REFERENCE: D01201 NUMBER: US/10/080,980
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 74
NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             latches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: wherein "N" is equal to "A", "C", "G" or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321 AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCAC 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1207 GCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGCCTGTAA 1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1087 GATTITTGGTTTTGTGGAAGGATTTTCCTTTGGCAAAAGAAGTCTTTTGGAGAAACTTTTGAATGA 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 TCCGCAGTTCCCAACTCCTTCCCTGAGGTGGTAGAGCTGAATGTCGGGGGTCAAGTTTAT 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           885 AAGCCGGGACCCCGACCGTCCCCCGGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 TTTACTCGCCATTCCACATTGATAAGCATCCCTCATTCCCTCTGTGGAAAATGTTTTCC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 TCCGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACGTGGGGGGGCCAGGTGTAC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 CGGCTCCTACACCATCGGGCGGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCG 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 104.6; DB 14; Length 688; Similarity 51.1%; Pred. No. 1.78-14; 92; Conservative 0; Mismatches 178; Indels 6;
                                                                                                                                                                                                                                     CTCATCGGTGACAGCATCTTT-----CATCAACCAATATACAGATGACAAGATCTGGTC 1320
                                      CCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACTTCGAGCTGCCA
                                                                                                       CCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAAGGGAAGCTGAATACTTCCAGCTCCCA 862
                                                                                                                                                                                 CGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAGCTCGTGCTG 419
                                                                                                                                                                                                                                                                                                                                                                                                             CCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGAC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGACCCGGCGCTGCACGGTGGTGTCGGTGCCCGACTCGCTGCTCTGGCGCATGTTCACG 305
                                                                                                                                                                                                                                                                                                                                    6;
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEO ID NOS: 38054
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 2311
LENGTH: 249
            Sequence 9, Application US/10056884

Publication No. US20030032786A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: K-betaM2

FILE REFERENCE: D0076 NP
CURRENT FILING DATE: 2002-01-24

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: US 50/263,872

PRIOR APPLICATION NUMBER: US 60/269,794

PRIOR APPLICATION DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR PRIOR PRICATION NUMBER: US 60/269,794

PRIOR APPLICATION NUMBER: US 60/269,794

PRIOR APPLICATION PRICA DATE: 2001-02-14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 161; Conservative
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SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1236 CAGAGTGTGGATTCCACATGGTGGCCTGTAACTCATCGGTGACAGCATCTTTCATCAACC 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AAGGAAGTGAAAGTGGGACTTCCTGGAATGAGCTCTTCACTTCCAGTTGGGACAGCCATT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AGAAATAGTATCACCTAAACAAGAACATGAAGATAGGATACATGACCAAGTCACTGATA 180
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Similarity 65.2%;
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NAME/KEY: misc feature
LOCATION: (1)...(425)

OTHER INFORMATION: n = A,T,C or G
US-09-834-975-451
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Best Local S
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Best Local
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PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BCOWN, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, I
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                              3347 TTTTATTGCGTGTGTGTGCATGTGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATG 3406
                                                                                                                  3287 CAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTG 3346
                                                                                                                                                                                             3227 AGACTTGTGCTACAAGAAGGTTAAAAGACCAGTTTTATTTTCAGCATTCCTCATGCATTT 3286
                                                                                                                                                                                                                                                                   3167 GTTAATAGCCATCCGTCCATGTAACTCTGTATTTTACTAAGGTACCAATAGCTCTTTCAT 3226
      141
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                                                                                                                                                       843 CTGAATACTTCCAGCTCCCA 862
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    Conservative
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100.0%; Pred. No. 3.1e-09
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                                                                                                                                                                                                                                US-09-925-299-112
                                                                                                                                                                                        Sequence 112, A
                                                                                                                                                                           GENERAL INFORMATION
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
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Application US/09925299 o. US20030040617A9

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; OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature; LOCATION: (1491); OTHER INFORMATION: n equals a,t,g, or C US-09-925-299-112
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Patent No. US20020055627A1
GENERAL INFORMATION:
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Best Local Similarity 70.2.
106; Conservative
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SEQ ID NO 112
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION UMMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER: OF SEQ ID NOS: 1556
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1487)
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                                    3438 АЛЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛАЛА 3468
                                                                        21 AA 20
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION UMMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION UMMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEO ID NOS: 8564
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Best Local S
Matches 106
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LOCATION: (8)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1487)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1497)
LOCATION: (1497)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                 PEARTURE:
NAME/KEY: misc_feature
LOCATION: (8)...(8)
OTHER INFORMATION: n equals a,t,9, or c
NAME/KEY: misc_feature
LOCATION: (1,488)...(1,488)
OTHER INFORMATION: n equals a,t,9, or c
NAME/KEY: misc_feature
LOCATION: (1,492)...(1,492)
OTHER INFORMATION: n equals a,t,9, or c
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publication No. US20
GENERAL INFORMATION:
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SEQ ID NO 1525
                                                 Query Match
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 112
      Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruben et al.
TITLE OP INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   LENGTH: 1493
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                                Local
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                                  Similarity
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. US20030109690A1
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Pred. No. 3.3e-08;
                 Score 79; DB 14;
Pred. No. 3.3e-08;
0; Mismatches 45
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                                                   DB 14; Length 1493;
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                   45; Indels
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                   0;
RESULT 14
US-09-770-444-872/c
Sequence 872, Application US/09770444
Patent No. US20020023280A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
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US-10-198-846-8619/c
; Sequence 8619, Application US/10198846
; Publication No. US20030099974A1
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: NK1-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT PILING DATE: 2002-07-18
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEO ID NOS: 14084
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 8619
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Best Local
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kat
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 15, 21, 25, 26, 29, 30, 33, 58, 59, 242, 243, 245, 247, 249, LOCATION: 266, 268, 279, 281, 282, 283, 285, 286, 287, 289, 290, 296, LOCATION: 297, 311, 312, 313, 324, 325, 326, 329, 331, 343, 344, 351, LOCATION: 352, 353, 361

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: 15, 21, 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                       3439 АДАДАДАДАДАДАДАДАДАДАДАДАДАДАДАД
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
UNDBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 872
LENGTH: 442
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US-09-739-254-66
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                                                                                                                                                                         APPLICANT: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PE032P1
CURRENT APPLICATION NUMBER: US/09/739,254
CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: 09/510330
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-25
EARLIER FILING DATE: 1999-08-25
EARLIER FILING DATE: 1998-08-25
                                                              EARLIER APPLICATION NUMBER: 60/0
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
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Best Local Similarity 64.9%;
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ORGANISM: Homo sapiens
                       LENGTH: 664
TYPE: DNA
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Kricker, Maja
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Haas, William David
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Ledford, Brooke L.
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Meaka, Joshua G.
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FEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equals a.t,9, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (63)
OTHER INFORMATION: n equals a.t,9, or c.
US-09-739-254-66
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Search completed: September 6, 2003, 11:49:24 Job time : 839 secs
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Best Local Similarity 64.0
Matches 110; Conservative
                                                                                     3357 TGTGTGTGCATGTGTGTATGTGTATCACAGGTAATAAAGGCAATTGGATGATTAAAAAA 3416
                                                                                                                                                                                                       2.1%; Score 74; DB 9; Length 664; 64.0%; Pred. No. 3.1e-07; ative 1; Mismatches 61; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                              Score
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Match Length DB ID
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Gapop 10.0 , Gapext 1.0
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13273.689 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est3:*
gb_est4:*
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28 AQ536411
11 AK015313
28 AQ525390
14 CA463745
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AQ536411 RPCI-11-3
AK015313 Mus muscu
AQ525390 HS_5228_B
CA463745 AGENCOURT
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ALIGNMENTS

RESULT 1
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863 GACTTGGTC 871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 TTTACTCGCCATTCCACATTGATAAGCATCCCTCATTCCCCTCTGTGGAAAATGTTTTCC 682
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                                                                                                              AK015313 810 bp mRNA linear HTC 05-DEC-200 Mus musculus adult male testis CDNA, RIKEN full-length enriched library, clone:4930434H12 product:inferred: RIKEN cDNA 4930434H12 gene / putative [Mus musculus], full insert sequence.

AK015313
                                    AK015313.1 GI:12853602
HTC; CAP trapper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTTTAAATCAAAATAGCAGCAGCAG 502
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/clone_lib="RPCI-11"
/note="Wyctor: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male_BAC_Library"
31 a 114 c 105 g 137 t 2 others
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Pred. No. 3.3e-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Tshi, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Pukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Feleischmann, W., Gastersland, T., Gissi, C., King, B., Kochiwa, H., Fleischmann, W., Gastersland, T., Gissi, C., King, B., Kochiwa, H., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, H., Aono, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, H., Aono, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, H., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerte, P., Nordone, P., Ring, B., Ringvald, M., Rodriguez, I., Sakamcto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibate, Y., Storoth, K. F., Suzuki, H., Sato, K., Shibate, Y., Storoth, K. F., Suzuki, H., Whitz, G., Wilming, L., Winshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDWAs

of 60,770 full-length cDWAs

Nature 420, 563-573 (2002)

6 (bases I to 810)

8 Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Pukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K.,
Hiracka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M.,
Koya, S., Kurihara, C., Mateuyama, T., Myazaki, A., Nishi, K.,
Koya, S., Kurihara, C., Mateuyama, T., Myazaki, A., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T.,
Tejina, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (10-UL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details.
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TAAGCAGCAAAAAAGCTGCGAAGGAAAAGCTCTCCATCGAGGAAGAGCTGGAGAAAT 523
                                TGAGCAGCAAAAAAAAAGCTGTTAAAGAAAAGCTCTCAATTGAGGAGGAGCTGGAGAAAT 1700
                                                                                                AGATGCGGCGGAAAAAGCGACTTACTCCGGATTCTGACTTCAGGCTCCAGGGGAATCGAACA 1646
                                                                                                                                                                        ACATCCAGACTCTGGACCGTCCCATCAAGAAGGGCCCTGTCCAGCTGATCCAACAGTCAG 1586
                                                                                                                                                                                                                     AGTCAGAGGCCAGCTCTCCGCAGGAGACGGTGATCTGTGGGCCTGTAACGCGCCAGAGCA 343
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                                                                       AGATGAGGCGGAAAAGTGACCTGCTCCGGACTCTGACGTCAGGCTCCAGGGAGTCGAACA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="maks"
/strain="C578L/6"
/strain="C578L/6"
/db_xref="MATOM_D8:4930434H12"
/db_xref="MATOM_D8:4930434H12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="inferred: RIKEN cDNA 4930434H12 gene / putative
[Mus musculus] (UniGene|Mm.46143, TIGR-MGI1|TC1870,
evidence: UG/TG1)"
/db xref="MGI:1914659"
/ - 192 c 208 g 184 t
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/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
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83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACEPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                             Plate: 804 row: F column: 10
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 592) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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HS_5228_BS_C05_T7A RPCI-11 Human Meale BAC Library Homo sapiens
genomic clone Plate=804 Col=10 Row=F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
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     157
                                                                                                                                                                                                                                                                                                                quality sequence stop: 592.
Location/Qualifiers
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                   /clone lib="RPCI-11 Human Male BAC Library"
/nothe="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen dd
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/clone="plate=804 Col=10 Row=F"
                                                                                                                                                                      /sex="male"
133 g
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
ERSION
EYWORDS
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CA463745
LOCUS
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Best Local Similarity
                                                                                                          Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 GCCAGATAGATACACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 CTTTGAAGATGCCTCCCAAGGAAGAGACACAAGAATGTGCCNCCTTTCCTCCGTGCTCCA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928 CTTTGAAGATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCCCTTCCCTGCTCCC 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: ggapbs-remail.nih.gov
Tissus Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA463745 784 bp mRNA linear ES' AGENCOURT 10724816 NIH MGC 169 Mus musculus CDNA clone IMAGE:6771233 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA463745
CA463745.1 GI:24920097
                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  Plate: LLCM3090 row: h column: 16
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                                                                                                                                              quality
/lab_host="DH10B (T1-phage-resistant)"
                     /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6771233"
                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 400.2; DB 28; Length 592; Pred. No. 7.6e-34;
                                                                                                                                                 втор: 456.
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Best Local
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                            1707 GTATCCAGGATTTCCTAAAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAAACATCCTT 1766
                                                                                                                                                                                                                        1647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1407 ACAAAGAAGGGGAGAGCGGCACGTCTTGCAATGACCTCTCCACATCTAGCTGCGACAGCC 1466
                                                                                      461
                                                                                                                                                                                                                                                                     341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 ACA---AAGGAGAGAGCGGCACCTCCTGCAATGACCTGTCCACTTCCAGCTGTGACAGCC
                                                                                                                                                                               401 TAAGCAGCAAAAAGAAAGCTGCGAAGGAAAAGCTCTCCATCGAGGAAGAGCTGGAGAAAAT
                                                                                                                                                                                                                                                                                                                                                              281 ACATCCAGACTCTGGATCGGCCCATCAAGAAAGGTCCGGTGCAGCTGATCCAACAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 AGTCAGAGGCCAGCTCTCCGCAGGAGACGGTGATCTGTGGGCCTGTAACGCGCCAGAGCA
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GGCAGTCTGAACTTTTACGGGAGTATCATCTATAGGGGGGGAGGCTGTGG
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                                                                                                                                                                                                                                                                     AGATGAGGCGGAAAAAGTGACCTGCTCCGGACTCTGACGTCAGGCTCCAGGGAGTCGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil
/ggccattatggcc); Site_2: Sfil (ggccgcctcggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-ARGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ARGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' Full-length
5'-ATTCTAGAGGCCGAAGGCGCCAACTG-dT(30)NN-3', Full-length
6'-ARGCAGTGGTATTY was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in thelaboratcory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

144 a 239 c 175 g 121 t
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; Pred. No. 8.5e-
0; Mismatches
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RESULT 5
BU961910
LOCUS
BU961910
BU961910
BU961910
AGENCOURT 10617166 NIH MGC 169 Mus musculus CDNA clone
IMAGE: 6742567 5', mRNA sequence.

BU961910
RACESSION
BU961910.1 GI:24191482
KEYMORDS
SOURCE
Mus musculus (house mouse)
SOURCE
Mus musculus (house mouse)
Bu43190.1 GI:24191482
FURANISM
BU43190.1 GI:24191482

REFERENCE
AUTHORS
Mus musculus (house mouse)
Bu43190.1 GI:24191482
FURANISM
BU43190.1 GI:24191482

REFERENCE
AUTHORS
NUS musculus (house mouse)
Bu43190.1 GI:24191482

REFERENCE
I (bases 1 to 778)

NACIONALI Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph. D.
Contact: Robert Strausberg, Ph. D.
Contact: Robert Strausberg, Ph. D.
CONALL Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I. M. A.G. E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation

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JE COUNT
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BY714867
                                                                       ACCESSION
VERSION
SOURCE
ORGANISM
                                                                                                                                           DEFINITION
                                                KEYWORDS
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Best Local :
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov plate: LLCM3080 row: n column: 06
                                          BY714867 mRNA
BY714867 RIKEN full-length enriched, aducDNA clone 4930434H12 5', mRNA sequence.
BY714867
BY714867 GI:27127984
EST.
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                                                                                                                                                                                                                                                                                               GGCAGTCTGAACTTTTACGGAAGTATCATCTATAGGGGGGGAGGGCTGTGGGG 651
                                                                                                                                                                                                                                                                                                                                    GGCAATCTGAACTTTTAAGGAAGTATCATCTATAAGGGAGGCTGGGGGCCG 1818
                                                                                                                                                                                                                                                                                                                                                                                             GTATCCAGGATTTCTTGAAGATAAAATTCCAGATCGCTTCCCTGAACGAAAACATCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGAGGCGGAAAAGTGACCTGCTCCGGACTCTGACGTCAGGCTCCAGGGAGTCGAACA
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musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="PHIOB (T1-phage-resistant)"
/clone lib="NIH MCC 169"
/clone lib="NIH MCC 169"
/clone lib="NIH MCC 169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil
/mote="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil
/ggccattatggcc); Site_2: Sfil (ggccgcctcggcc); GDNA made
by oligo-dT priming and directionally cloned. 5 and 3'
adaptors were used in cloning as follows:
5'-ANGCACTGGTATCAACGCAGAGTGGCCATTACGGCCGGC3' and
5'-ANGCACTGGTATCAACGCAGAGTGGCCATTACGGCCGGCGAGATG-GT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in thelaboratory of M.
Brownstein (NIMH, NIH). Noce: this is a NIH_MGC Library."
26 a 180 C 199 g 160 t 13 others
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/clone="IMAGE:6742567"
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'mol_type="mRNA"
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0; Mismatches 6
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Mammalia; Eutheria; Rodentia; Schurognath; Muridae; Muridae; Mus. (CE) 1 (bases 1 to 952)

RES Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Subuki, H., Yamanaka, I., Kiyosawa, H. Yagi, K., Tomatu, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomatu, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Cobani, J., E., Cousins, S., Dalla, E., Dragani, T.A., Hit, D.P., Bult, C., Hume, D.A., Ogaekenbush, J., Schinial, L.M., Kanapin, A., Matsuda, H., Batalov, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Varyis, E.D., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltasi, L., Martchonni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.T., Reed, J.T., Red, D.J., Reid, J., Ring, B.Z., Ringvald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sakazumishi, A., Yoshino, M., Waterston, R., Lander, K., Shiragawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, K., Shiragawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, K., Shiragawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, S., Rodess, S., Sakazume, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Maki,K., Matahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                       Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-45-503-9216
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                                                                                                                                                                                                                              Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                  visit our web site (http://genome.gsc.riken.go.jp) for
Location/Qualifiers
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Query Match
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                                                                                                                                                                                                                                                 1827 АААААААGAGTCATTTTGAAATTAACCTCATAAAAGGAATTCATATTTTAAAGGAAAA 1886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 GTGAGCCTTCCCGGTGGTCCTCCTCTCATTGTGACTGCTGCTGCAAGAATGGCAAGGGAG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                        GTATCCAGGATTTCCTAAAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAACATCCTT 1766
                                                                                                                                                 AATACAACTAATGATGCACATTTCTTAGAACACAATAGTCCATTGATATACTACTGCCTA 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGCGGCGGAAAAGCGACTTACTCCGGATTCTGACTTCAGGCTCCAGGGAATCGAACA 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA---AAGGAGAGCGGCACCTCCTGCAATGACCTGTCCACTTCCAGCTGTGACAGCC
                                                            GGCAGTCTGAACTCTTACGGGAGTATCATCTATAGGGGGAGGCGTGCGGGCG------ 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAGCAGCAAAAAGAAAGCTGCGAAGGAAAAAGCTCTCCATCGACGAAGAGCTGGAGAAAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGCAGCAAAAAAAAGCTGTTAAAGAAAAGCTCTCAATTGAGGAGGAGCTGGAGAAAT 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGAGGCGGAAAAGTGACCTGCTCCGGACTCTGACGTCAGGCTCCCGGGAGTCGAACA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATCCAGACTCTGGATCGGCCCATCAAGAAAGGTCCGGTGCAGCTGATCCAACAGTCAG 403
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                          CTTTGNCTA-CCCTCCTTAACGTGCCACTCACAGGGCACACTTTTTTTATATGTGGATCA 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="testis"
'dev_stage="adult"
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db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bento-soares@uiowa.edu

The sequence contained an ollgo-dT track that was present in the oligonucle-gctide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized testis library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this CDNA sequence: 1-35, >POLY_A#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .cr: 319 335 8250
Fax: 319 335 9565
Email: bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF391086
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EST
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UI-R-CA1-bcd-a-05-0-UI.sl UI-R-CA1 Rattus norvegicus cDNA clone
UI-R-CA1-bcd-a-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
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Mammālia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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                             Similarity
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a
                                                                                                                                                                                                                                                                                       /clome lib="UJ-R-CA1"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco R; The UJ-R-CA1
plibrary is a subtracted library derived from the following
tissues: thalamus, cerebllum, hypothalamus, medulla, pons
midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
site at ratest.eng.uiowa.edu.
                                                                                                                                        TAG_TISSUE=testis
TAG_SEQ=ACGCAG"
111 c
                                                                                                                                                                                                                      site at ratest eng.uiowa.edu. The previously described in (Bonaldo, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-CA1
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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/clone="UI-R-CA1-bcd-a-05-0-UI"
/lab host="DH10B (Life Technologies)"
/clone_lib="UI-R-CA1"
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                          9.8%;
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   Indels 16; Gaps
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AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE	TITLE JOURNAL MEDLINE PUBMED PERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE	RESULT 8 AK043351 LOCUS DEFINITION ACCESSION VERSION VERSION VERWORDS SOURCE ORGANISM		Db 483 Qy 11473 Db 423 QY 1533 QY 1533
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Mitshi, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	Garninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 9279253 10349636 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramassu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 1042159 3	AKO43351 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730087N02 product:hypothetical protein, full insert sequence. AKO43351 AKO43351: GI:26335652 HTC; CAP trapper. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mus musculus at the control of the control	GGGGAAAAAGCGACTTACTCCGGATTCTGACTTCAGGCTCCAGGGAATCGAACATGAGCA	
CDS .	COMMENT . FEATURES SOURCE	TITLE	TITLE JOURNAL MEDLINE PUBNED REFERRICE AUTHORS TITLE JOURNAL REFERENCE	AUTHORS
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Krakawa, J., Shihngawa, A., Shibhta, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fakuda, S., Ailawa, K., Izawa, M., Nishi, K., Kyosawa, H., Kondo, S., Yamanda, I., Saito, T., Oshachi, Y., Gojobori, T., Bono, H., Kashikawa, T., Saito, R., Kadoca, K., Matsuda, H., Kojobori, T., Bono, H., Kashikawa, T., Saito, R., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Maranda, H., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Kadoca, K., Matsuda, H., Ashburmer, M., Baralov, S., Casavant, T., Saito, R., Kadoca, K., Matsuda, H., Kadoca, K., Matsuda, H., Kadoca, K., Matsuda, H., Kadoca, K., Matsuda, H., Kadoca, K., Maranda, M., Kadoca, K., Matsuda, H., Kohisuk, H., Magher, L., Mashika, J., Mazaralii, J., Monbeete, P., Nordone, P., Siig, B., Kadoca, K., Matsuda, M., Kazaralii, J., Monbeete, P., Nordone, P., Siig, B., Kadoca, K., Matsuda, M., Kazaralii, J., Monbeete, P., Nordone, P., Siig, B., Kadoca, K., Matsuda, K., Hasegawa, Y., Kawaji, H., Kohisuki, S., and Hayashidaki, Y., Voshida, K., Hasegawa, Y., Kawaji, H., Kohisuki, S., Siili, P., Siili, Y., Tinckani, K., Mamzari, H., Matsuda, T., Hori, F., Siili, Y., Siili, Y., Kondo, S., Komo, H., Kawai, H., Kawai, J., Kojian, Y., Kondo, S., Komo, H., Kawai, H., Kawai, J., Kojian, Y., Kondo, S., Komo, H., Kawai, H., Kawai, J., Kojian, Y., Kondo, S., Komo, H., Kawai, H., Kawai, J., Kojian, Y., Kondo, S., Komo, H., Kawai, M., Koya, S., Katiki, K., Manzaki, A., Mutta, M., Kangawa, I., Kawai, A., Matsuda, T., Takaka, H., Matsuda, T., Takaka, H., Matsuda, M., Kangawa, I., Kawai, A., Matsuda, M., Kangawa, I., Kawai, A., Matsuda, T., Takaka, A., Matsuda, A., Matsuda, T., Takaka, A., Matsuda, T., Takaka, A., Matsuda, A., Matsuda, A., Matsuda, A., Matsuda, A., Matsuda, A., Matsuda,
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GCCTGTAACTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTACAGAGGATCCTGGACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGA 1078
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                                                                                   AAGTTCACCTACTTGGAGCAGGCGTTCGATCGACTGTCTGAGGCCGGCTTCCACATGGTG
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SYTTVRDNOADAKFRRVARINVCGRIALAKEVFGDTLNESEDDRQPEKYTSRFYLKF
TYLEOAFDRLSEAFFHWVAGNSGGTAAFWQYRDDKUWSSYTEYIFFREPQKIVSPRQ
TYLEOAFDRLSEAFFHWVAGNSGGTAAFWQYRDDKUWSSYTEYIFFREPQKIVSPRQ
EHEDRKRROKYTDKGSESGTSCNELSTSSCDSHSEASTPQDNPANTQQAAAHQPNTLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK047519 2343 bp mRNA linear HTC 05-DEC-2002 Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930082J01 product:hypothetical protein,
Shibata,K., Iroh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Iroh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yamamoto,R., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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JOURNAL
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                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-res@gec.riken.go.jp, URLihttpi//genome.gc.riken.go.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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/organism="Mus musculus"

/mol type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:B930082J01"

/db_xref="taxon:10090"
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1319 TCAAGCTACACTGAATATGTCTTCTACCGTGAGCCT----TCCAGATGGTCACCCTCACAC 1379
1352 AGCAGTTÁCÁCTGAÁTÁCATCTTCCTTCCGACCACCTCAGAAAÁTÁGTGTCÁCCCAAGCAA 1411
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RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Pukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casawant, T., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuchiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Quackenbush, J., Schrinil, L.M., Staubli, F., Suzuki, R., Tomita, M., Quackenbush, J., Schrinil, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Erownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Rang, B., Ringyald, M., Rodriguez, I., Sakanto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Stoch, K., Suzuki, H., Shiming, L., Wonshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Shiming, L., Wonshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Shiman, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kamaya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kaniya, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kawaji, H., Kohtsuki, S., and Jawa, Shima, Y., Kawaji, H., Kohtsuki, S.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

6 (bases 1 to 2584)
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Please visit our web site for further details.
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/note="unnamed protein product; hypothetical protein
                                                       /dev_stage="adult"
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/mol_type="mRNA"
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                         AAGTTCACCTACTTGGAGCAGGCGTTCGATCGACTGTCTGAGGCCGGCTTCCACATGGTG
                                                     AAATTCAAGCACCTGGAAAGGGCTTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTG 1258
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Shibata,K., Itoh,M., Aizawa,K.,
Konno,H., Akiyama,J., Nishi,K.,
Sumi,N., Ishii,Y., Nakamura,S.,
Yamamoto,R., Matsumoto,H., Sakag
                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new common Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKO42569 mRNA linear HTC Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-enriched library, clone:A730006K23 product:hypothetical
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igh-efficiency full-length cDNA
eth. Enzymol. 303, 19-44 (1999)
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Eutheria; Rodentia;
  a,K., Nagaoka,S., Sasaki,N., Carninci,P.
i,K., Kitsunai,T., Tashiro,H., Itoh,M.,
a,S., Hazama,M., Nishine,T., Harada,A.,
Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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linear HTC 05-DEC-2002 A, RIKEN full-length

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegre.riken.go.jp, URLihttp://genome.gsc.riken.go.jp/, Tel-45-503-9222, URLihttp://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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URL:http://fantom.gsc.riken.go.jp/.
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Please visit our web site for further details.
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     844 GGTGTCAGTGGTAGTCGGTGGTGGCAGCGCTCCGGACAAGCGCTCTGGGTTCCTCACC 903
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                                                                                                                                                                                                                CTGGGCTACCGTGGCTCTTACACCACGGTGCGAGATAACCAGGCAGATGCCAAGTTCAGG 963
                                                                                                                                                                                                                                                                                 GTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGGGGACAGGCAGATGCCAAGTTTCGG 1075
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FTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPOKIVSPK GSHEDRRADKVTDKGSESGTSCTSLSTSSCDSHSBASTPQNPAYTGQAAAHQPNTLT LDRESRKAFVQQMAPPDKRRRNSLFJGSLISKSRETNLSKKKVCEKLSVEEEMKKCIQD LDRESRKAFVQMAPPDRKRRNSLFJGSLISKSRETNLSKKKVCEKLSVEEEMKKCIQD KKKIHLPDCFPERRQWGSELLOKYGL"
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/dev_stage="7 days neonate"
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/db_xref="GI:26335191"
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Email: ggapbs-remail.nih.gov
Tissus Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAAATTCCAGATCGGTTTCCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTA 1783
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                                                                                                                                                        2312 TGACTCCGTATGCATGAGTATTTGTG----CAACACAAGCACTAAGTATGTATATACA 2368
                                                                                                                                                                                                                                                                                  2254 --GGGGGGAATGGCAGATTTATATGACTTTTCACTCAAATCTATATGTGCCAGTTTATAT 231:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2142 ---CTCTCATCCTTCTACCTCCTCCTTTGA--ATGAGGGTATGGTAGAAAAAGATCTGG 2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2046 CGTCCCATGTGCTAACTATCTT-ATATATAATGAGAGCCAGCTACGTAAAAGTAGCTGAG 2104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1808 GCTGGGGGGGGGAAAAAAAAAAAAAAGAGTCATTTTGAAATTAACCTCATAAAAGGAAT 1867
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                                                                                                                                                                                                                                                                                                                                                                      524 CCCGGTGGCTTATGTTAAGAAATTATCCTTTTCCCTTTTCCTTTTGTTTATGGGGTT 583
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                                                                                                       644 TGACTTTGTATGCATGAGCCGTTCTGACACAAGCACAGTATATGTCTGTATATATGCACA
                                                                                                                                                                                                                                            584 GAGGGGAGAATGGCAAATTTGTATGATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGATATACTACTGCCTACTTTACCTAGTTCACCTTAACATGTAAATCCACAGGGTAGA 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGATGTACTACTTCCCTACTTTGCCTAGCTCACCTTAACGTGTAAATCCACAGGGTAGA 283
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/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="IMAGE:6310836"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 129"
/clone_lib="NIH MGC 129"
/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector: olfactory 
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Pred. No. 2
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2.4e-24;
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                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CB 1 (bases 1 to 319)

CB (bases 1 to 319)

RS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Goodyne,J.D., White,O., Sutton,G., Blake,J.A., Baraddon,R.C., Man-Wai,C., Clayton,R.A.,C., M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmazos,S.M., Merrick,J.M., Shirley,R., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Filllys,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,B.J., Bulmke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon, M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2605 CTTTGTCTGCATTAAGAGAGGATGAGGAGA 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2545 AACAAATTGTATTCCTTATTGTGAAATTAATACCCTCAGGCTCCATTTTACTGCTTTGCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2489 AAGATTTCCCAGCCTTTCTT----CACAACACTTTCTAACATCAAATGACTCTCATCATC 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA332022
BST35911 Embryo, 8 week I
AA332022
AA332022.1 GI:1984264
                                                                                                                                                                                                            Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-114 (1995)
                                                                                                                                                                                                         Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTTCCCCACCTAAAGAACCTGGGGAAA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAATTCCCTTCCTAATTTGAAAAAAAAAACCCCCCAGGCTCCCTTGGAAATAATAAGG 938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAATGCACACGACCTAAGGGC--TGGACAGCAGAGGGCTAACATCTTACTATCAGCTG
                                                                                                                                                                                                                                                                                                                                                                     Institute for Genomic Research
2 Medical Center Drive, Rockville, MD 20850 USA
/mal type="manua"
/db_xref="ATCC (inhost):133650"
/db_xref="caxon:9606"
/db_xref="caxon:9606"
/dev_sfeage="embryo, 8 wks"
/clone lib="Embryo, 8 week I"
/clone lib="Embryo, 8 weeks; Vector: pBluescript SK-;
                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                 Location/Qualifiers
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Homo sapiens cDNA 5' end,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

RES (1 dbases 1 to 424)

RES (2 document), Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D., P., Bult, C., Hume, D.A., Ouackenbush, J., Schrimil, L.M., Kanapin, A., Metsuda, H., Batalov, S., Dalla, E., Cousins, S., Dalla, E., Dragani, T.A., Pletcher, C. F., Forrest, A., Frazer, K.S., Gaastevaland; T., Garbioldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hickawa, N., Jackson, I. J., Jarvis, E.D., Kanai, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Magashima, T., Numata, K., Okido, T., Pavan, W. J., Pertca, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ringwald, M., Sandelih, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomata, M., Verardo, R., Wagner, L., Wahlesteedt, C., Wang, Y., Wang, Y., Vang, Y., Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1842 TTTGAAATTAACCTCATAAAAGGAATTCATATTTTAAAGGAAAAAAATACAACTAATGAT 1901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8Y706433 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 1700026A08 5', mRNA sequence.

BY706433 BY706433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCTCATCCTTCTACCTC 2159
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Best Local :
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1467 AGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCATCTGTGGTCCCGTGACACGCCAGACCA 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
S., Hashizume,W., Hayyashida,K., Hirozame,T., Hori,F., Imotani,K.,
Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S.,
Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library, Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Nature 420, 563-573 (2002)
22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                              n 8.3%;
Similarity 82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                               /note="Site 1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, adult male testis"
/note="5ite_1: XhoI; Site_2: BamHI; cDNA library was
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/dev_stage="adult"
/lab_host="SOLR"
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strain="C57BL/6J"
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                                                                                                                                                                                                                        cDNA was cloned into the XhoI and BamHI sites. 98 c 114 g 79 t
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                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequence Genome Res. 10 (11), 1757-1771 (2000)
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422 bp mRNA linear HTC 05-DEC-200 Mus musculus adult male testis CDNA, RIKEN fill-length entiched library, clone:1700026A08 product:inferred: RIKEN CDNA 4930434H12 gene / putative [Mus musculus], full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 422)
6 (bases 1 to 422)
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/mol_type="mRNA"
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/db_xref="MGI:0900"
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/clone Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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Search completed: September 6, 2003, 08:44:53 Job time : 6362 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                               699.2
423.4
319.4
                                                                                                                                                                                 Score
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Match
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1. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

6. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

6. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1991.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1992.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1993.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1994.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1995.DAT:
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/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1995.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA1999.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA2001.DAT:
/SIDS1/gcgdata/genesed/geneseqn-emb1/NA2001B.DAT:
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/SIDS1/gcgdata/genesed/geneseqn-emb1/NA2001B.DAT:
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Human K+betaM2 cDN Novel human coding Human BAC ACO06652 Human CDNA encodin Human CDNA encodin Human TRICH-15 cDN Human pancreatic c Human pancreatic c
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	11	22	297	2.1	2	5
Human prostate exp	ABV48988	23	346	2.1	72.6	44
Human SLC7 related	T1735	25	1814		73	3
П	013	22	348	٠	73	42
Human secreted pro	694	21	~		73.2	41
polyn	881	22	4055	2.1	73.4	40
colon car	493	22	4	•	73.4	39
prostate	ABV44911	23	375		73.4	8
secreted	AAC59836	21	1204		73.6	37
prostate	74	22	1992		73.8	36
encoding ma	503	25	1091		73.8	35
ZmGnsN1-1	AAC89723	22	1091		73.8	34
	633	21	664	٠	74	33
	AAC59297	21	887		74.2	32
Human cervical can	110	22	655	٠	74.2	31
Arabidopsis thalia	1	24	442		75	30
DNA encoding novel	ABK43528	23	1856	٠	75.2	29
Drosophila melanog	ABL06734	23	2847	٠	76.2	28
Drosophila melanog	ABL06735	23	847	٠	76.2	27
Human polynucleoti	ABL90605	24	2796		76.8	26
	ABL90331	24	1493	٠	79	25
Human colon cancer	AAH34433	22	1493		79	24
Human colon cancer	AAC98102	21	1492		79	23
Human secreted pro	AAC60033	21	1119		79	22
Human cancer agent	AAS60450	22	425		79	21
Antisense oligonuc	AAD46069	24	80		80	20
Oligonucleotide fo	ABQ13667	24	1757		95.8	19.
Oligonucleotide fo	ABQ13666	24	1757		95.8	18
σ	ABT09813	24	688		104.6	17
Oligonucleotide fo	ABQ40657	24	854		108.6	16
Oligonucleotide fo	ABQ40656	24	854		108.6	15
Oligonucleotide fo	ABQ13669	24	1757		109.8	4
Oligonucleotide fo	σ	24	1757		109.8	13
Oligonucleotide fo	ABQ40655	24	854	ω .ω	114.2	12
Oligonucleotide fo	065	24	854	ω .ω	114.2	11
Human osteoblast d	81	24	109201	4.8	167	10
Polynucleotide enc	981	24	2052	4.8	167	9

ALIGNMENTS

AAD46068 standard; cDNA; 3468 BP. 27-DEC-2002 (first entry)

Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder; reproductive disorder; metabolic disorder; premature puberty; nephritis; endocrine disorder; memory disorder; neuroendocrine condition; asthma; spermatogenesis; renal disease; learning deficiency; Alzheimer's disease; neurodegenerative disease; proliferative disorder; autoimmune disease; carcinoid tumour; blood coagulation disease; blood platelet disease; rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy; graft-versus-host disease; organ rejection; antisterility; thrombolytic; antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive; nephrotropic; cytostatic; nootropic; hypotensive; vulnerary; gene; ss. Location/Qualifiers 515..1801 /*tag= a /product= "Human K+betaM2 protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human potassium channel beta-subunit CC (K+betaM2) proteins and polynucleokides encoding such proteins. The CK+betaM2 sequences are useful for diagnosing, treating and/or preventing CC reproductive disorders, neural disorders, disorders related to aberrant CC potassium regulation or hyper potassium channel activity, metabolic CC disorders (e.g. premature pubsetty), endocrine disorders (e.g. aberrant CC growth hormone synthesis and/or secretion), memory disorder, disorders (e.g. spermature pubsetty), endocrine disorders (e.g. aberrant to condition related to aberrant thyroid hormone release, renal disease or disorders (e.g. comphritis), disorders related to aberrant higher brain function (e.g. CC learning deficiencies), neurodegenerative diseases or disorders (e.g. asrhma). CC They may be used to modulate haemostatic or thrombolytic activity, to cc diseases, wounds, autoimmune diseases or disorders, blood platelet diseases, wounds, autoimmune diseases, disorders sethma), organ rejection cor graft-versus-host disease, and hyperproliferative diseases. K+betaM2 CCM, k+betaM2 cDNA.
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Matches 3468
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14-FEB-2001; 2001US-269794P.
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                                                           CATCCAGGGTTTAAACTACTTTTTCAGCATCACCTTCACCTGTGGACTCTTATACATTTTG
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                                  CATCCAGGGTTTAAACTACTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG
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                                                       TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGGAGAGCGGCACGTCTTGCAATGA
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CCAAGGGCTGTGCTCCCCAGCAGCCCTCTCTTAGAATATTTCAGATGGATG	TICACICAAATCTATATGTGCCAGTITATATTGACTCCGTATGCATGAGTATTTGTGCAA 2340	CTCCTTTGAATGAGGTATGGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAATTT 2220 [TACTTCGTCCCATGTGCTAACTATCTTATATATATGAGAGCCAGCTACGTAAAAGTAGC 2100	ATAGTICATIGATATACTACTGCCTACTTTACCTAGTTCACCTTAACATGTAAATCCACA 1980	AGGAAGGCCTGGGGGAAAAAAAAAAAAAAAAAAAAAATATAACCTCATAA 1860	، أن با با	1620 1620 1680 1680	CTESTCCCCTGACACCCAGACCAGACTCCAGACTCTGGACCGTCCCATCAAGAAGGGG1560 DI
RESULT 2 ABN59764 Standard; cDNA; 2412 BP. XX ABN59764; AC ABN59764; XX DT 28-JUN-2002 (first entry) XX XX DE Novel human coding sequence SEQ ID NO: 175. XX XX KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;		321 ANAGATAATTAATAATTAATAAGTGGGGGCAAGCACTCCTAATTTGGTTTTATTGCGTGTG 321 AGAAGATTATTATTATTTTCAGCATTCCTCATGCATTTCAGTGGTAACCAAA 321 AGAAGATTATTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG 3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTG	3121 TITICANTACATCC IN ACTIVITATION CONTROLLY AND ACADAM CINTERNACION CONTROLLY AND ACTIVITATION CONTROLLY AND ACTIVITACION CONTR	301 CGGCCTTTGCCTGTGCCATGCTAGATTTAGCTTGTATCTTATGATGTCTGTACA	2881	2761 GAGTTCTTACTG 2821 GTGTTCCTGTGT 2821 GTGTTCCTGTGT 2881 TTTTGTTTGTTT	2641 CAAACATTĆCTTGTGTTAAAAAATCAAACATTCATATCCACAAAATTTTCTGCTAAATG	2581 2581

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Best Local Similarity
Matches 1645; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTm). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. rhexitson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Zhou P, Asundi V, Zhang J,
Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
expressed sequence tag; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
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The present invention relates to human potassium channel beta-subunit (K+betaM2) proteins and polynucleotides encoding such proteins. The CC (K+betaM2) exquences are useful for diagnosing, treating and/or preventing the conductive disorders, neural disorders, disorders related to aberrant potassium regulation or hyper potassium channel activity, metabolic condisorders (e.g. premature puberty), endocrine disorders (e.g. aberrant cycleotion endocrine disorders disorders (e.g. premature puberty), neuroendocrine condition related condition related to aberrant thyroid hormone spermatogenesis), neuroendocrine condition related condernant thyroid hormone release, renal disease or disorders (e.g. capanitis), disorders related to aberrant higher brain function (e.g. capanitis), disorders related to aberrant higher brain function (e.g. capanitis), disorders related to aberrant thyreid muscle tone or excitability (e.g. Alzheimer's condition proliferative disorders (e.g. carcinoid tumour) and disorders (e.g. disease), proliferative disorders (e.g. carcinoid tumour) and disorders conducted to modulate haemostatic or thrombolytic activity, to the property of the provent blood coagulation diseases or disorders, blood platelet
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                                                                                                                                                                                                                                                                                                                                                                                             reproductive, neurar, disorders or diseases
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                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 349-350; 366pp; English.
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14-FEB-2001; 2001US-269794P.
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                                                                                                                                                                                                                                                                                                                                                                                                                       potassium channel beta-subunit, K+betaM2, proteins and nucleic ds, useful for diagnosing, treating and/or preventing e.g. roductive, neural, metabolic, endocrine, memory, neurodegenerative
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RESULT 4 ABA09216/c ID ABA09216; XX AC ABA09216; XX . DT 11-JAN-20

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TGGCAAAAGAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGA

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11-JAN-2002

(first entry)

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TGGCAAAAGAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGA 1161
                                                                                                                                                                                                    AAGATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCCTTCCTCCCTGCTCCCTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGACAGAGATGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAACTCCTTCCCTGAGGTGGTAGAGCTGAATGTCGGGGGTCAAGTTTATTTTACTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATGGCTCTGAGTGGAAACTGTAGTCGTTATTATCCTCGAGAACAAGGGTCCGCAGTTC
                                            GACAGGCAGATGCCAAGTTTCGGAGAGTTCCCCGGATTTTGGTTTGGAAGGATTTCCT
                                                                 GACAGGCAGATGCCAAGTTTCGGAAGAGTTCCCCCGGATTTTTGGTTTTGTGAAGGATTTTCCT 1112
                                                                                                           ACCGCAAGTGGGGTTTCATTACTGTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGG 660
                                                                                                                                          ACCGCAAGTGGGGTTTCATTACTGTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGG 105
                                                                                                                                                                             AAGATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCCTTCCTCCCTGCTCCCTGCCG
                                                                                                                                                                                                                                              AACTCCTGACCCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGCCACAGTGACTTTG
                                                                                                                                                                                                                                                                             AACTCCTGACCCCCGATGAAATCAAGCCAAAAGCCCAGATGAATTCTGCCACAGTGACTTTG 932
                                                                                                                                                                                                                                                                                                            TTCCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCA 480
                                                                                                                                                                                                                                                                                                                                             TTCCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCA 872
                                                                                                                                                                                                                                                                                                                                                                               ACACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGACAGAGATGGAT
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Pred. No. 6
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Sequences ABB10991-ABB12330 represent 1350 novel human polypeptides, and CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a cC nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of iderecting the nucleotides or polypeptides in a sample, and methods of ideritiying compounds which to polypeptides of the invention have homology to known proteins, thereby cC giving an insight into their probable biological activities, and hence cc polypeptides of the invention have homology to known proteins, thereby can activities, including cyrokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; immunomodulatory activity; activin or inhibin related activities; chemotactic or chemokinetic activities; tissue growth activities; or may be conditions, e.g., by protein or gene therapy. Such conditions or cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoiethy, achievacers (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoiethy activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoiethy activities, polypeptides and nucleotides of the inventions and conditions or architish), protein or gene therapy. Such conditions architish, concerned the such conditions of a chivity and activities and and annormal conditions or activities and unlease.

CC archaers (e.g., of burns, incisions and ulcers), while those with the such to be activitied to conditions or activity may be used to promo
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 844-845; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-457740/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uman proteins and DNA encoding sequences useful for preventing, reating or ameliorating a medical condition in a mammalian subject \cdot.g. arthritis and cancer -
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 906 BP; 220 A; 225 C; 216 G; 245 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       546 CTCCTGACCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGCCACAGTGACTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
AGATACACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTG 1226
                                                                                                                                     CAGGCAGATGCCAAGTTTCGGAGAGTTCCCCGGATTTTGGTTTGGGAAGGATTTCCTTG 1114
                                                                                                                                                                                   GATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCCTTCCTCCCTGCTCCCTGCCGAC 427
                                                                                                                                                                                                                                                                                     GATGCCTCCCAAGGAAGCGACACAAGAATCTGCCCCCCTTCCTCCCTGCCCCGAC 994
                                                                                                                                                                                                                                                                                                                                            CTCCTGACCCCCGATGAAATCAAGCAAAGCCCAGATGAATTCTGCCACAGTGACTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                        CCAGAAAAAGGAAGACTGAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAAAAAGGAAGACTGAAAAAGGGAAGCTGAATACTTCCAGCTCCCAGACTTGGTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCACATTGATAAGCATCCCTCATTCCCTCCTGTGGAAAATGTTTTCCCCCAAAGAGAGAC
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                                               GCAAAAGAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCCTGATCGAGCCCCAGAA
                                                                              GCAAAAGAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCAGAA 1174
                                                                                                                CAGGCAGATGCCAAGTTTCGGAGAGTTCCCCCGGATTTTGGTTTGTGGAAAGGATTTCCTTG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGGCTAATGATCTAGCCAAGGACTCCAAGGGAAGGTTTTTCATTGACAGAGATGGATTC
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Pred. No. 4.6e-129;
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AAS34230
ID AAS3
XX
AC AAS3
XC AAS3
XX
DT 17-I
XX
DE Huma
XX
KW Humm
KW immu Human cDNA encoding a novel foetal antigen, SEQ ID No 754. 17-DEC-2001 AAS34230 standard; cDNA; (first entry)

AGATACACCTCCAGATTTTATCTCAAATTCAAGCACCTAATGGGGGCACCTG 195

Human; foetal tissue antigen; ss; antiinflammatory; neuroprotective; immunomodulator; cardiovascular; cytostatic; nephrothropic;

ZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	222
Cerebral 1 Schaller (Cerebral 1) Schaller (Cerebra 1) Schaller (cardiovascular; autoimmu hyperproliferative disor cardiovascular disorder;
Alzheimer at ischaemaa; anglogenesis; Alzheimer; a disease; infection; oc wound healing; epithelial cell pro wound healing; epithelial cell pro Homo sapiens. 17-JAN-2001; 2000US-013021. 17-JAN-2000; 2000US-013065. 16-PEB-2000; 2000US-018658. 16-PAR-2000; 2000US-018658. 16-PAR-2000; 2000US-018659. 16-PAR-2000; 2000US-019813. 19-PAR-2000; 2000US-019813. 19-PAR-2000; 2000US-029867. 20-JUN-2000; 2000US-021648. 10-JUL-2000; 2000US-021648. 10-JUL-2000; 2000US-021885. 11-JUL-2000; 2000US-021885. 11-JUL-2000; 2000US-021886. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021887. 11-JUL-2000; 2000US-021889. 11-JUL-2000; 2000US-022558. 11-JUC-2000; 2000US-022558. 11-JUC-200	ar; autoimmune d rative disorder; ar disorder; car
lesis, nervous system ton; ocular disorder; ell proliferation; fo	disease; rheumatoi ; breast neoplasm; rdiac arrest; cere
	rheumatoid arthritis neoplasm; cancer; est; cerebrovascular
disorder infection, additive.	itis; ; ; ; ; ; ;
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25-SEP 2000; 26-SEP 2000; 27-SEP 2000; 27-SEP 2000; 29-SEP 2000; 29-SEP 2000; 29-SEP 2000; 29-SEP 2000; 20-OCT 2000; 20-OC	SEP-2000
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 754; 642pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins are given in the specification. The present sequence
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                                                                                                                                                                                                                                                                                                                                         1902 GCACATTTCTTAGAACACAATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTCAC
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DB; AAU21410.
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435; Conserv
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                         CCAGCTACGTAAAAAGTAGCTGAGAGGCCTTGGGAGTCATTTATCCCAAACTGGG-TTTTT
                                                                                                   CTTAACATGTAAATCCACAGGGTAGATTTCTTTCTAGATGTGGAAGTACAAGAAAATCTT
                                                                                                                                                                                                                                     GCACATTTCTTAGAACACAATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTCAC
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; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2000US-0259678.
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Pred. No. 1.7e-74;
0; Mismatches 4; Indels 1;
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RESULT 6
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12-APR-2001; 2001US-283440P.
20-APR-2001; 2001US-28592P.
27-APR-2001; 2001US-28763P.
04-MAY-2001; 2001US-288666P.
18-MAY-2001; 2001US-293742P.
25-MAY-2001; 2002US-293744P.
22-JAN-2002; 2002US-351107P.
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       The invention relates to human transporters and ion channels (TRICH) polypeptides and mucleic acid molecules according such polypeptides. TRICH proteins are useful for preparing compositions for diagnosing of treating treating compositions for changes of conditions associated with decreased expression or overexpression of functional TRICH e.g. atherosclerosis or cancer invention is useful in gene therapy. The present sequence is
                                                                                                                                                                                                                 Swarnakar A, rac
Swarnakar A, Lee EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TRICH-15 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD49513;
                                                                                                                    New human functional transporters and ion channels (TRICH) polypeptides, useful for preparing a composition for diagn treating a disease associated with decreased expression or overexpression of TRICH e.g. cancer
                                                                                                                                                                                                                                Foreythe IU, L. Lu DAM, Gandhi AR, Lu DAM, Yao M
                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002WO-US11760
                                                                                             Claim 5; Page 200-201; 204pp; English.
                                                                                                                                                                                   WPI; 2003-092996/08.
P-PSDB; AAE32081.
                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
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 TRICH
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, Lu Y, Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
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/product= "Human T
114..230
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231..1532
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/product= "Mature human TRICH protein"
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Tang YT, Yue H, .Raumann BE, Lal PG, Azinza
Thornton M, Nguyen DB, Arvizu CS, Emerling
J, Ding L, He A, Griffin JA, Sanjanwala MM;
, Xu Y, Au-Young JK, Das D, Lee SY, Chang.H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel; TRICH; atherosclerosis; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRICH
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                                                                                                                                      diagnosing ion or
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Query Match 9.2%; Score 319.4; DB 25; Length 2398. Best Local Similarity 58.0%; Pred. No. 9-54; Matches 769; Conservative 0; Mismatches 466; Indels 90;
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CTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCATC 1501
                                                                      GATAGGAAACATGACAAAGTCACTGATAAAGGAAGTGAAAGTGGGACTTCCTGTAATGAG 1175
                                                                                                                                                                                                                                                                                                                                                        CACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGCCTGTAAC 1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTCCCCTCTGTGGAAAATGTTT 679
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                                                                                                             TGCTGCAAGAATGGCAAAG---GTGACAAAGAAGGGGGAGAGCGGCACGTCTTGCAATGAC 1441
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31-JAN-2001; 2001US-265682P.
09-FEB-2001; 2001US-267568P.
21-MAR-2001; 2001US-2875651P.
28-APR-2001; 2001US-287112P.
16-MAY-2001; 2001US-291631P.
12-JUL-2001; 2001US-305484P.
27-NOV-2001; 2001US-3333626P.
The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour; gene; ss.
                                                                                    Claim 1; SEQ ID NO 4467; 300pp + Sequence Listing; English.
                                                                                                                              New isolated polynuclectide and pancreatic tumor polypeptides, for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer
                                                                                                                                                                                                                                                          Benson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2002; 2002WO-US02781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic cancer expressed cDNA SEQ ID NO 4467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV99059 standard; cDNA; 632
                                                                                                                                                                                                                WPI; 2002-627435/67.
                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV99059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1236 AGTGCCCAGCAGGCAACAGCTCACCAACCTAACACTTTAACATTGGATCGCCCCTCTAAA 1295
                                                                                                                                                                                                                                                       DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGATCGGTTTCCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCAT 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCTCATCAGCAAGTCCCGGGAAACAAATCTGTCCAAAAAGAAA-----GTCTGTGAG 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGCCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAAGCGACTTACTCCGG 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGGTCCCGTGACA-----CGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAG 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATA 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCTAAGTGTGGAAGAAATGAAAAAGTGTATTCAGGATTTTAAAAAAATCCACATT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGCACCTGTACAATGGATACCCCCACCAGACAAACGCAGAAACAGTGAACTCTTTCAG 1355
                                                                                                                                                                                                                                                     Kalos MD,
                                                                                                                                                                                                                                                       Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                     Persing DH,
                                                                                                                                                                                                                                                       Hepler WT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc contiguous residues of (a); (d) sequences that hybridize to (a), under cc domestic stringent conditions; (e) sequences having at least 75% or 90% cidentity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and can tigen presenting cells expressing the polypeptide are useful in creating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid polynucleotides can be used as probes or primers for nucleic acid polynucleotides can be used as probes or primers for nucleic acid in this ting expression, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the unour cells, in vaccines and for gene therapy.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO can at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                    30-JAN-2001; 2001US-265305P.
31-JAN-2001; 2001US-265682P.
09-FEB-2001; 2001US-27568P.
21-MAR-2001; 2001US-278651P.
28-APR-2001; 2001US-287112P.
16-MAY-2001; 2001US-391631P.
12-JUL-2001; 2001US-305484P.
20-AUG-2001; 2001US-313999P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 632 BP; 178 A; 92 C; 119 G; 239 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic cancer expressed cDNA SEQ ID NO 564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV95156 standard; cDNA; 614 BP
Benson DR,
                                                                                                                                                                                                                                                     30-JAN-2002; 2002WO-US02781.
                                                                                                                                                                                                                                                                                           08-AUG-2002
                                                                                                                                                                                                                                                                                                                               WO200260317-A2.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; tumour; gene;
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                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3206 AGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAGACCAGTTTTATT 3265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3266 TTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGT 3325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 GGTAATAAAGGCAATTGGATGATATCTGTAGGAGGAAAACAATGACTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AGGTACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAGACCAGTTTTATT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 5.9%;
Similarity 93.4%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCCAAGCACTCCTAATTTGTTTTATTGCGTGTGTGTGCATGTGTGTATGTGTATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAGCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGT 134
  Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
  Lodes
                                                                                                                                                                                                                                                                                                                                                                                                    88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 205; DB 24;
Pred. No. 3.4e-31;
0; Mismatches 15;
  3
Persing
  DH,
Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 632;
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  Jiang
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CC any of a group of over 4000 nucleotide (1) comprising: (a) (C) any of a group of over 4000 nucleotide sequences (ABV99628-ABV99145); (C) by complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under CC contiguous residues of (a); (d) sequences that hybridize to (a), under CC contiguous residues of (a); (d) sequences that hybridize to (a), under CC (ABF6859-ABF6863) encoded by (1) and oligonucleotide can be used to CC detect cancer in a patient and compositions comprising polypeptides, CC polynucleotides, antibodies, fusion proteins, T cell populations and CC antigen presenting cells expressing the polypeptide are useful in CC treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid chybridisation, in the design and preparation of ribozyme molecules for CC inhibiting expression of the tumour polypeptides and proteins in the CC uncer: The sequence data for this patent did not form part of the printed concer: The sequence data for this patent did not form part of the printed concer: The sequence data for this patent did not form part of the printed concert in the concert of the printed concert of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and pancreatic tumor polypeptides, of diagnosing, preventing and/or treating cancer, particularly pancreatic cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 564; 300pp + Sequence Listing; English
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밁 ફ 뭉 Ś В ર્ 밁 Ś Matches 210; Query Match Best Local 9 Sequence 614 BP; 177 A; 87 C; 110 G; 236 T; 4 other; 3270 GCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGTGTGC 3329 3210 ACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAAGACCAGTTTTATTTTCA 3269 181 121 61 μ. Similarity 93.3%; ACCAATAGCTCTTTCATAGACTTGTGCTACAAGAAGGTTAAAAAGACCAGTTTTATTTTCA GCATTCCTCATGCATTTCAGTGGTAACCAAAAAATAATTTGTCAATTAATAGTTGTGTGC <u>ATAAAGGCAATTGGATGATATCTGTAGGAGGAAAACAATGACTAA</u> Conservative 0; Score 201; DB 24; Length 614; Pred. No. 2.1e-30; Mismatches 15; Indels 0 Gaps 120 60 0

RESULT 9 ABT09812 standard; cDNA; 2052

05-DEC-2002 (first entry) .

Polynucleotide encoding the K+beta M6 protein SEQ ID No 1.

Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine; sedative; gynaecological; potassium channel beta subunit; K+betaM6; gastrointestinal; reproductive; neural; sleep; low DNA repair capacity; hyperpotassium channel activity; cardiovascular; melatonin synthesis; mammary cancer tunourigenesis; pineal gland associated disorder; pulmonary disorder; immune disorder; NF-kB activity; migraine headache; low free-radical buffering capacity; delayed sleep phase syndrome; circadian cycle; melatonin secretion; cancer; gene; ss.

WO200270727-A2

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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide encoding a potassium channel beta subunit (K-betaM6) polypoptide or its variants. The human potassium beta subunit polynucleotide or polypoptide is useful for diagnosing, preventing, treating or ameliorating a pathological condition such as gastrointestinal, reproductive, neural sleep, cardiovascular or pulmonary disorders, a disorder related to hyperpotassium channel activity, an immune disorder related to aberrant NF-kB activity, pineal gland associated disorders, migraine headaches, disorders associated with aberrant melatonin synthesis and/or release or with low DNA repair capacities or low free-radical buffering capacity, delayed sleep phase syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis, age related disorders associated with decreased melatonin secretion, or cancer. This polynucleotide sequence represents the cDNA encoding the potassium channel beta subunit (K-betaM6) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding human potassium channel beta subunit polypeptide, useful for diagnosing, preventing, treating or ameliorating e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2052 BP; 380 A; 640 C; 607 G; 425 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2001; 2001US-270132P.
27-MAR-2001; 2001US-278953P.
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                                                                                                                                                                                                                                                                                                                        1147
                                     1321 AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCAC 1373
1065 CAGCTACACCGAGTACGTCTTCTGCAGGGAGTGAGCTCCCCAGACCCCCCTCGC 1117
                                                                                                                                                                                                                           1207 GCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGCCTGTAA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 AGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGTTCCCCCG 1086
                                                                                                                                                                                                                                                                             885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         967 CCCCCCTTCCCTGCCTGCCCGACCGCAAGTGGGGTTTCATTACTGTGGGTTACAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-713455/77.
                                                                                                                                                                                                                                                                                                                                                                   825 CATCACCGTTTGCGGAAAGACGTCGCTGGCCAAGGAGGTGTTTGGGGGACACCCTGAACGA 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                GATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAAGAAGTCTTTGGAGAAACTTTGAATGA 1146
                                                                                  CTCCACGGGCACCTGCGCCTTTGCCAGCAGCAGCCAGAGCGAGGACAAGATCTGGAC
                                                                                                                                                                                                                                                                           AAGCCGGGACCCGACCGTCCCCCGGAGCGCTACACCTCGCGCTATTACCTCAAGTTCAA 944
                                                                                                                                                                                                                                                                                                                   AAGCAGAGACCCTGATCGAGCCCCCAGAAAGATACACCTCCAGATTTTATCTCAAATTCAA 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGCCGTCCCAGTCGCTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCG
                                                                                                                                CTCATCGGTGACAGCATCTTT-----CATCAACCAATATACAGATGACAAGATCTGGTC 1320
                                                                                                                                                                             CTTCCTGGAGCAGGCCTTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCTCCTACACCATCGGGCGGACGCGCAGGCGGACGCCAAGTTCCGGCGAGTGGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%;
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Pred. No. 1.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 140;
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RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC (a) screening modulators of precursor stem cell differentiation into CC osteoblasts, or bone tissue deposition;
CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of CC osteoblast formation or osteoporosis; or CC (c) treating or monitoring treatment of the conditions cited in (b), or CC (c) treating or monitoring treatment of the conditions cited in (b), or CC (c) treating or monitoring treatment; of the conditions cited in (b), or CC (c) treating or monitoring treatment; of the conditions cited in (c), or conditions include postmenopausal osteoporosis, glucocorticoid consceptored or male osteoporosis, osteopenia, osteodystrophy, conditions conscipations or male osteoporosis, osteopenia, osteodystrophy, conditions conscipations of the involve altered bone metabolism (e.g. idiopathic juvenile costeoporosis), skeletal disease linked to breast cancer, mastcoytosis, conditions syndrome or fibrous dysplasia. The present sequence is that of an CC osteophast differentiation associated cDNA marker of the invention.

CC Note: The sequence data for this patent did not form part of the printed condition, but was obtained in electronic format directly from WIPO creating and the condition of the invention.

CC Active the condition of the condition of the invention of the invention of the condition of the
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                                                                                                                                                                                                                                                                                                       Query Match 4.8%; Score 167; DB 24; Length 109201; Best Local Similarity 64.6%; Pred. No. 3.5e-23; Matches 267; Conservative 0; Mismatches 140; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109201 BP; 32871 A; 23488 C; 22108 G; 30734 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 32; 78pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000US-255882P
24-APR-2001; 2001US-285691P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human osteoblast differentiation related cDNA SEQ ID NO 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to genes and their expression profiles are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              process
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001; 2001WO-US48276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO
1087. GATTTTGGTTTGTGGAAGGATTTCCTTTGGCAAAAGAAGTCTTTTGAATGA
                                                                                                                                                                                                      9291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Axelrod DW, Cook JS,
                                                                                       CGGCTCCTACACCATCGGGCGGGACGCGCAGGCGACGCCAAGTTCCGGCGAGTGGCGCG
                                                                                                                              AGGATCCTGCACCTTGGGCAGAGAGAGGGCAGACGCCAAGATTTCCGGAGAGTTCCCCG
                                                                                                                                                                                                  CACGCCGTCCCAGTCGCTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCG
                                                                                                                                                                                                                                                   CCCCCTTCCTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGGTTACAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Einstein R,
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                          9172
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RESULT 11
ABQ40654
ID ABQ40
XX ABQ40
AC ABQ40
AC ABQ40
DT 12-JU
XX Oligo
KW Human
KW drug;
KW Gastr
KW SNP;
XX Homo
XX Homo
XX Homo
PN WO200
PN WO200
PN O1-SE
PR 01-SE
PR 01-SE
PR 01-SE
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            This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridized to two classes, each with at least one completely of the degree of hybridized to tho classes is determined from the call on the amplicon. From the ratio of labels hybridized to the two classes is determined from the condition of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory conditions of sufferentiation of religion condition of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide collour particularly by detecting mutation. The method allows the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytosine methylation; 5'. CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide for detecting cytosine methylation SEQ ID NO 27245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ40654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2001; 2001WO-EP10074.
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCAC 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCTACACCGAGTACGTCTTCTGCAGGGAGTGAGCTCCCCAGACCCCCTCGC 8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCACGGGCACCTGCGCCTTTGCCAGCAGCAGCGACCAGAGCGAGGACAAGATCTGGAC 8932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCTGGAGCAGGCCTTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAG 8992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACCTGGAAAGGGCTTTTGATATGTTGTCAGAGTGTGGATTCCACATGGTGGCCTGTAA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCCGGGACCCCGACCGTCCCCCGGAGCGCTACACCTCGCGCGCTATTACCTCAAGTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCATCGGTGACAGCATCTTT-----CATCAACCAATATACAGATGACAAGATCTGGTC 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCAGAGACCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAAATTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCACCGTTTGCGGAAAGACGTCGCTGGCCAAGGAGGTGTTTGGGGGACACCCTGAACGA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 854 BP; 131 A; 98 C; 289 G; 336 T; 0. other;
                                                                                                                1241
                                                                                                                                                                                          1181
                                                                                                                                                                                                                                                                    1121 GAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCCAGAAAGATAC 1180
                                                                                                                                                                                                                                                                                                                                                                                                                              1001 TGGGGTTTCATTACTGTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCA 1060
                                      1295
                                                                                                                                                                                                                                                                                                                                                1061 GATGCCAAGTTTCGGAGAGTTCCCCCGGATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAA 1120
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791. GATTAGAGCGAGGATAAGAÍTTÍGGATTAGTTÁTATCGAGTÁCGÍTTÍTTÍGTAGGGAG
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                                                                                                                                                                                                                                                                                                          GACGTTAAGTTTCGGCGAGTGGCGCGTATTATCGTTTGCGGAAAGACGTCGTTGGTTAAG 610
                                   CAATATACAGATGACAAGATCTGGTCAAGCTACACTGAATATGTCTTCTACCGTGAG 1351
                                                                                                             TGTGGATTCCACATGGTGGCCTGTAACTCATCGGTGACAGCATCTTT-----CATCAAC 1294
                                                                                                                                                                                       ACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAG 1240
                                                                          TCGGGTTTTTATATGGTGGCGTGTAGTTTTACGGGTATTTGCGTTTTTGTTAGTAGTATC 790
                                                                                                                                                    ATTTCGCGTTATTATTTTAAGTTTAATTTTTTGGAGTAGGTTTTCGATAAGTTGTTCGAG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854;
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RESULT 12
ABQ406
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ABQ406
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05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 27246
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                                                                                                                                                                                                                                                                                                                                            Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2001; 2001WO-EP10074.
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2000DE-1044543.
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Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis; comprises selective hybridization amplicons from chemically treated DNA -

Claim 12; 56pp + Sequence Listing; 56pp; German

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RESULT 13
ABQ13668
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Best Local :
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                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 854 BP; 336 A; 289 C; 98 G; 131 T; 0 other;
     WO200218632-A2
                                                                                                                                                                                                           Oligonuclectide for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                        ABQ13668 standard; DNA; 1757 BP.
                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1295 CAATATACAGATGACAAGATCTGGTCAAGCTACACTGAATATGTCTTCTACCGTGAG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1061 GATGCCAAGTTTCGGAGATTCCCCGGATTTTGGTTTGGGAAGGATTTCCTTTGGCAAAA 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 GACGTTAAGTTTCGGCGAGTGGCGCGTATTATCGTTTGCGGAAAGACGTCGTTGGTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 TCGGGTTATATTATCGGTTATCGCGGTTTTTATATTATCGGGCGGACGCGTAGGCG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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Similarity 59.7%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAG 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATAC 1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTGGATTCCACATGGTGGCCTGTAACTCATCGGTGACAGCATCTTT------CATCAAC 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTCGCGTTATTATTTTAAGTTTAATTTTTTGGAGTAGGTTTTCGATAAGTTGTTCGAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGTGTTTGGGGGATATTTTGAACGAAAGTCGGGATTTCGATCGTTTTTCGGAGCGTTAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGGTTTTTATATGGTGGCGTGTAGTTTTACGGGTATTTGCGTTTTTGTTAGTAGTATC 65
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 114.2; DB Pred. No. 3.6e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 854;
                                                                                                                                                                                                                 NO 259.
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                                              ABQ13669 standard; DNA; 1757
ABQ13669;
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12-JUL-2002

(first entry)

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This invention describes a novel method for determining the degree of commethylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide nucleic acid (PNA) oligomers and the degree of hybridisea to two classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Amagolation-Amagolatiz represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in cyclosine methylation described in the described in the disclosure of the invention.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1757 BP; 246 A; 209 C; 640 G; 662 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-371829/40.
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05-SEP-2000; 2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
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                                                                          1241
                                                                                                                                                          1665
                                                                                                                                                                                                                                                                                                                    1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1061 GATGCCAAGTTTCGGAGAGTTCCCCGGATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAA 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1545 GACGTTAAGTTTCGGCGAGTGGCGCGTATTATCGTTTGCGGAAAGACGTCGTTGGTTAAG 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                 GAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATAC 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                      reregarrecacareereeccreraacrearee 1273
                                                                                                                                                     ATTTCGCGTTATTATTTTAAGTTTAATTTTTTGGAGTAGGTTTTCGATAAGTTGTTCGAG
                                                                                                                                                                                                                  ACCTCCAGATTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAG 1240
                                                                                                                                                                                                                                                                                                                    GAGGTGTTTGGGGATATTTTGAACGAAAGTCGGATTTCGATCGTTTTTCGGAGCGTTAT 1664
TCGGGTTTTTATATGGTGGCGTGTAGTTTTACG 1757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 109.8; DB 24; Length 1757;
62.6%; Pred. No. 3.1e-12;
rative 0; Mismatches 102; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guetig D;
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Oligonucleotide for detecting cytosine methylation SEQ ID NO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC methylation of a particular cytosine in a motif 5. Cpg-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide nucleic acid (PNA) oligoners CC member, of oligonucleotides and/or peptide nucleic acid (PNA) oligoners CC and the degree of hybridiseation to both classes is determined from the CL label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of cherapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

CC Ampliance of the invention of the sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Sim:
Matches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-371829/40.
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1757 BP; 662 A; 640 C; 209 G; 246 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                     1181
                                                                                                                          1121
                                                                                                                                                                                                         1061 GATGCCAAGTTTCGGAGAGTTCCCCGGATTTTGGTTTGTGGAAGGATTTCCTTGGCAAAA 1120
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                               GAGGTGTTTGGGGGATATTTTGAACGAAAGTCGGGATTTCGATCGTTTTTCGGAGCGTTAT 94
                                                                                                                          GAAGTCTTTGGAGAAACTTTGAATGAAAGCAGAGACCCTGATCGAGCCCCAGAAAGATAC 1180
                                                                                                                                                                                                                                                      ACCTCCAGATTTTATCTCAAATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCAGAG 1240
                                                                                                                                                                    GACGTTAAGTTTCGGCGAGTGGCGCGTATTATCGTTTGCGGAAAGACGTCGTTGGTTAAG 154
                                                                                                                                                                                                                                                                                            TGGGGTTTCATTACTGTGGGTTACAGAGGATCCTGCACCTTGGGCAGAGAGGGGACAGGCA 1060
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                            Score 109.8; DB 24; Length 1757; Pred. No. 3.1e-12;
                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                                                                                                           Indels
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967 CCCCCCTTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGGTTACAG 1026

Query Match Best Local :

Similarity Conservative

3.1%; 57.1%;

Score 108.6; DB 24; Length 854; Pred. No. 4.6e-12; 0; Mismatches 159; Indels 6;

6

Gaps

0

Sequence 854 BP; 132 A; 98 C; 302 G; 322 T; 0 other;

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RESULT 15
ABQ40656/c
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                            This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridised to two classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of classes of oligoners, the degree of methylation is calculated. The method CC classes of oligoners, the degree of methylation is calculated. The method CC is used; (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mucations or single nucleotide comply and (ii) for differentiation of cell or tissue comply and continuestigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Associated for determining the degree of cytosine methylation described in cc check of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA \, -
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; 56pp + Sequence Listing; 56pp; German.
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158 CTTCO 1267 CTCAT 98 CTCCA 1321 AAGCT 38 CAACT	218 AAACCGAAA 207 GCACCTGGA	278 CATCACCO	398 CACGCCC 1027 AGGATCC	1
CTCAT	AAACCGAAA GCACCTGGA	CATCACCO AAGCAGAO	CACGCCC AGGATCC	1
CITCCTHARACCHACCTTCGACAACTATCCGAATCGAACTTCCACATAATAACGTACAA 99 CTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC 1320 [CATCACCGTTTACGAAAAAACGTCGCTAACCAAAAAAATATTTAAAAACACCCTAAACGA 219 AAGCAGAGACCCTGATCGAGCCCCAGAAAGATACCTCCAGATTTTATCTCAAATTCAA 1206	CACGCCGTCCCAATCGCTAAACGACAACCGACGCTCGAACTACATCACCATCGACCATCGACCTACCG 339 AGGATCCTGCACCTTGGGCAGAGGGACGGCAGATGCCCAAGTTTCCGAGAGAGTTCCCCG 1086	

Search completed: September 5, 2003, 15:10:11 Job time: 850 secs